GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:26:09 ; Search time 165 Seconds
(without alignments)
625.478 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	3	US-09-840-989A-2	Sequence 2, Appli
2	1268	100.0	247	3	US-09-361-736-10	Sequence 10, Appl
3	1268	100.0	247	4	US-10-116-051-2	Sequence 2, Appli
4	1268	100.0	247	4	US-10-177-293-441	Sequence 441, App
5	1268	100.0	247	4	US-10-418-226-10	Sequence 10, Appl
6	1268	100.0	247	4	US-10-465-572-18	Sequence 18, Appl
7	1268	100.0	247	4	US-10-372-683-41	Sequence 41, Appl
8	1268	100.0	247	4	US-10-614-990-2	Sequence 2, Appli
9	1268	100.0	247	5	US-10-723-860-4202	Sequence 4202, Ap
10	1268	100.0	247	5	US-10-824-075-2	Sequence 2, Appli
11	1268	100.0	247	6	US-11-068-678-3	Sequence 3, Appli
12	1268	100.0	247	6	US-11-076-158-2	Sequence 2, Appli
13	1268	100.0	247	6	US-11-125-206-10	Sequence 10, Appl
14	937	73.9	276	3	US-09-925-300-1426	Sequence 1426, Ap
15	662.5	52.2	256	3	US-09-840-989A-3	Sequence 3, Appli
16	662.5	52.2	256	4	US-10-614-990-3	Sequence 3, Appli
17	660.5	52.1	204	4	US-10-116-051-10	Sequence 10, Appl
18	660.5	52.1	204	6	US-11-076-158-10	Sequence 10, Appl
19	628	49.5	170	3	US-09-361-736-9	Sequence 9, Appli
20	628	49.5	170	4	US-10-418-226-9	Sequence 9, Appli
21	628	49.5	170	6	US-11-125-206-9	Sequence 9, Appli
22	358	28.2	70	3	US-09-864-761-37770	Sequence 37770, A
23	354	27.9	293	5	US-10-900-423-13	Sequence 13, Appl
24	354	27.9	302	3	US-09-193-881-23	Sequence 23, Appl
25	354	27.9	302	4	US-10-177-293-443	Sequence 443, App
26	354	27.9	302	4	US-10-338-395-23	Sequence 23, Appl
27	354	27.9	302	4	US-10-418-226-12	Sequence 12, Appl
28	354	27.9	302	4	US-10-364-889-4	Sequence 4, Appli
29	354	27.9	302	4	US-10-295-027-100	Sequence 100, App
30	354	27.9	302	4	US-10-173-999-80	Sequence 80, Appl
31	354	27.9	302	4	US-10-058-270A-22	Sequence 22, Appl
32	354	27.9	302	4	US-10-712-124-20	Sequence 20, Appl
33	354	27.9	302	5	US-10-789-378-74	Sequence 74, Appl
34	354	27.9	302	6	US-11-125-206-12	Sequence 12, Appl
35	351.5	27.7	251	4	US-10-418-226-2	Sequence 2, Appli
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37	333.5	26.3	251	3	US-09-361-736-2	Sequence 2, Appli
38	303	23.9	118	4	US-10-116-051-9	Sequence 9, Appli
39	303	23.9	118	6	US-11-076-158-9	Sequence 9, Appli
40	111	8.8	40	5	US-10-900-423-3	Sequence 3, Appli
41	99	7.8	40	5	US-10-900-423-2	Sequence 2, Appli
42	95.5	7.5	299	4	US-10-282-122A-49895	Sequence 49895, A
43	94.5	7.5	415	4	US-10-425-115-320042	Sequence 320042,
44	92	7.3	1010	4	US-10-425-115-312927	Sequence 312927,
45	91	7.2	901	3	US-09-828-062-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-840-989A-2
; Sequence 2, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Ti
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247
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RESULT 2
US-09-361-736-10
; Sequence 10, Application US/09361736

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; Patent No. US20020102634A1
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/361,736
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,529
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-361-736-10

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  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 3
US-10-116-051-2
; Sequence 2, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-051-2

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  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 4
US-10-177-293-441
; Sequence 441, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Gannavarpu, Manjula
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Mertens, Maureen
;  APPLICANT:  Myer, Vic
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Monahan, John
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Bast Jr., Robert C.
;  APPLICANT:  Hortobagyi, Gabriel N.
;  APPLICANT:  Pusztai, Lajos
;  APPLICANT:  Meric, Funda
;  APPLICANT:  Sahin, Aysegul
;  APPLICANT:  Mills, Gordon B.
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
;  TITLE OF INVENTION:  PREVENTION, AND THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-038
;  CURRENT APPLICATION NUMBER: US/10/177,293
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,887
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/301,572
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;  PRIOR FILING DATE: 2001-06-27
;  PRIOR APPLICATION NUMBER: US 60/306,501
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/325,002
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/362,585
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/xxx,xxx
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 506
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 441
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-177-293-441

  Query Match             100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 5
US-10-418-226-10
; Sequence 10, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Stanniocalcin-Alpha
;  FILE REFERENCE: PF143P1D2
;  CURRENT APPLICATION NUMBER: US/10/418,226
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 09/361,736
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: 08/460,529
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/ US94/13206
;  PRIOR FILING DATE: 1994-11-30
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: human
US-10-418-226-10

  Query Match             100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 6
US-10-465-572-18
; Sequence 18, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
;  APPLICANT: Riggins, Gregory
;  APPLICANT:  Lal, Anita
;  TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
;  FILE REFERENCE: 000250.00012
;  CURRENT APPLICATION NUMBER: US/10/465,572
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US/10/201,642
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/307,600
;  PRIOR FILING DATE: 2001-07-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-465-572-18

  Query Match             100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 7
US-10-372-683-41
; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
```

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;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-41

  Query Match            100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 8
US-10-614-990-2
; Sequence 2, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
;  FILE REFERENCE: PF108P2
;  CURRENT APPLICATION NUMBER: US/10/614,990
;  CURRENT FILING DATE:  2003-07-09
;  PRIOR APPLICATION NUMBER: US/09/840,989A
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/29432
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-614-990-2

  Query Match            100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 9
US-10-723-860-4202
; Sequence 4202, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4202
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-4202

  Query Match            100.0%;  Score 1268;  DB 5;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 10
US-10-824-075-2
; Sequence 2, Application US/10824075
; Publication No. US20050026829A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.,
;  APPLICANT:  HONGO, JO-ANNE S.
;  APPLICANT:  ZLOT, CONSTANCE H.
```

```
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SELECTIVE MODULATION OF VASCULARIZAT
;  FILE REFERENCE: P2014R1
;  CURRENT APPLICATION NUMBER: US/10/824,075
;  CURRENT FILING DATE:  2004-04-14
;  PRIOR APPLICATION NUMBER: US 60/463,226
;  PRIOR FILING DATE: 2003-04-16
;  NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-824-075-2

  Query Match             100.0%;  Score 1268;  DB 5;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 11
US-11-068-678-3
; Sequence 3, Application US/11068678
; Publication No. US20050152837A1
; GENERAL INFORMATION:
;  APPLICANT: Recipon, Herve
;  APPLICANT:  Macina, Roberto A.
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Sun, Yongming
;  TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring, Staging,
;  TITLE OF INVENTION:  Imaging and Treating Cancer
;  FILE REFERENCE: DEX-0087
;  CURRENT APPLICATION NUMBER: US/11/068,678
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: US/09/705,500
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/163,444
;  PRIOR FILING DATE: 1999-11-04
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-068-678-3

  Query Match             100.0%;  Score 1268;  DB 6;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 12
US-11-076-158-2
; Sequence 2, Application US/11076158
; Publication No. US20050208552A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/11/076,158
;  CURRENT FILING DATE:  2005-03-10
;  PRIOR APPLICATION NUMBER: US/10/116,051
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: PRIOR  APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-076-158-2

  Query Match             100.0%;  Score 1268;  DB 6;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 13
US-11-125-206-10
; Sequence 10, Application US/11125206
; Publication No. US20050208569A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen, Henrik
```

```
;  APPLICANT:  et al,
;  TITLE OF INVENTION: Human Stanniocalcin-Alpha
;  FILE REFERENCE: PF143P1D3
;  CURRENT APPLICATION NUMBER: US/11/125,206
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: 10/418,226
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 09/361,736
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: 08/460,529
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/ US94/13206
;  PRIOR FILING DATE: 1994-11-30
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: human
US-11-125-206-10

  Query Match             100.0%;  Score 1268;  DB 6;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-121;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 14
US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
;   LENGTH: 276
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (43)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (273)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (275)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

  Query Match             73.9%;  Score 937;  DB 3;  Length 276;
  Best Local Similarity   99.5%;  Pred. No. 6.8e-87;
  Matches  185;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 148

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 208

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 268

Qy        181 SLMEKI 186
              ||||||
Db        269 SLMEXI 274


RESULT 15
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
;  FILE REFERENCE: PF108P2
;  CURRENT APPLICATION NUMBER: US/09/840,989A
;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/29432
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

  Query Match             52.2%;  Score 662.5;  DB 3;  Length 256;
  Best Local Similarity   53.4%;  Pred. No. 6.4e-59;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
              :|| :||  || |   :   :      |      |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


Search completed: April  4, 2006, 14:29:48
Job time : 167 secs
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WO 0055174

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:27:09 ; Search time 25 Seconds
(without alignments)
300.766 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	354	27.9	302	7	US-11-051-720-1458	Sequence 1458, Ap
2	308	24.3	187	7	US-11-051-720-1402	Sequence 1402, Ap
3	93.5	7.4	350	6	US-10-533-811-31	Sequence 31, Appl
4	85.5	6.7	311	6	US-10-793-626-2460	Sequence 2460, Ap
5	83	6.5	319	6	US-10-793-626-792	Sequence 792, App
6	83	6.5	319	6	US-10-793-626-2008	Sequence 2008, Ap
7	83	6.5	344	7	US-11-096-568A-27671	Sequence 27671, A
8	83	6.5	365	7	US-11-096-568A-27670	Sequence 27670, A
9	83	6.5	398	6	US-10-793-626-44	Sequence 44, Appl
10	83	6.5	398	6	US-10-793-626-1498	Sequence 1498, Ap
11	82.5	6.5	1724	7	US-11-096-568A-32051	Sequence 32051, A
12	82.5	6.5	1730	7	US-11-096-568A-32050	Sequence 32050, A
13	82.5	6.5	1757	7	US-11-096-568A-32049	Sequence 32049, A
14	82.5	6.5	2535	7	US-11-096-568A-27511	Sequence 27511, A
15	81.5	6.4	2518	7	US-11-096-568A-27512	Sequence 27512, A
16	81	6.4	4384	6	US-10-821-234-1120	Sequence 1120, Ap
17	78.5	6.2	2376	7	US-11-096-568A-27513	Sequence 27513, A
18	77.5	6.1	762	6	US-10-204-639-21	Sequence 21, Appl
19	76.5	6.0	1087	7	US-11-096-568A-27941	Sequence 27941, A
20	75.5	6.0	364	7	US-11-072-512-2127	Sequence 2127, Ap
21	75	5.9	357	7	US-11-072-512-2525	Sequence 2525, Ap
22	75	5.9	750	7	US-11-072-512-2432	Sequence 2432, Ap
23	75	5.9	1333	7	US-11-096-568A-27668	Sequence 27668, A
24	75	5.9	1351	7	US-11-096-568A-27667	Sequence 27667, A
25	75	5.9	1528	7	US-11-096-568A-27666	Sequence 27666, A
26	74.5	5.9	292	7	US-11-096-568A-10393	Sequence 10393, A
27	74.5	5.9	401	7	US-11-096-568A-10392	Sequence 10392, A
28	74.5	5.9	406	6	US-10-821-234-1113	Sequence 1113, Ap
29	74.5	5.9	698	7	US-11-038-901-2	Sequence 2, Appli
30	74	5.8	625	7	US-11-072-512-2061	Sequence 2061, Ap
31	74	5.8	857	7	US-11-096-568A-24558	Sequence 24558, A
32	74	5.8	867	7	US-11-096-568A-24557	Sequence 24557, A
33	74	5.8	903	7	US-11-096-568A-24556	Sequence 24556, A
34	74	5.8	1149	7	US-11-110-082-30	Sequence 30, Appl
35	73	5.8	1148	7	US-11-110-082-29	Sequence 29, Appl
36	73	5.8	1373	7	US-11-096-568A-29856	Sequence 29856, A
37	73	5.8	1391	7	US-11-096-568A-29855	Sequence 29855, A
38	73	5.8	1568	7	US-11-096-568A-29854	Sequence 29854, A
39	72.5	5.7	224	7	US-11-096-568A-10357	Sequence 10357, A
40	72.5	5.7	278	7	US-11-096-568A-10356	Sequence 10356, A
41	72.5	5.7	292	7	US-11-096-568A-29657	Sequence 29657, A
42	72.5	5.7	292	7	US-11-096-568A-33082	Sequence 33082, A
43	72.5	5.7	402	7	US-11-096-568A-29656	Sequence 29656, A
44	72.5	5.7	402	7	US-11-096-568A-33081	Sequence 33081, A
45	72.5	5.7	414	7	US-11-096-568A-16419	Sequence 16419, A

ALIGNMENTS

RESULT 1
US-11-051-720-1458
; Sequence 1458, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHOD
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1458
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1458

Query Match 27.9%; Score 354; DB 7; Length 302;
Best Local Similarity 32.4%; Pred. No. 2.9e-27;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

```
Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::          ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: : :    |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::| ||| | ::|: |: |   | |::  :   :  |  ||  || | |:    |
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL---------------- 222
              |:  :   |  ||  ||      | | |   |:   :  ||
Db        192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy        223 KVLLRNLRGEEDSPSH 238
              :   |  :||  | ||
Db        252 RETGRGAKGERGSKSH 267
```

RESULT 2
US-11-051-720-1402
; Sequence 1402, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:

```
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1402
;   LENGTH: 187
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1402

  Query Match             24.3%;  Score 308;  DB 7;  Length 187;
  Best Local Similarity   37.6%;  Pred. No. 5.3e-23;
  Matches   59;  Conservative   37;  Mismatches   49;  Indels   12;  Gaps    3;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::         ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :      |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSN 157
              ::::| ||| | ::|: |: |   | |::    || :
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMI----HFKD 164


RESULT 3
US10-533-811-31
; Sequence 31, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Valenzuela, Jesus G.
;  APPLICANT:  Ribeiro, Jose M.C.
;  APPLICANT:  Barral, Aldina
;  APPLICANT:  Netto, Manoel
;  APPLICANT:  Brodskyn, Claudia
;  APPLICANT:  Gomes, Regis
;  TITLE OF INVENTION: LU. LONGIPALPIS POLYPEPTIDES AND METHODS OF USE
;  FILE REFERENCE: 4239-67028-08
;  CURRENT APPLICATION NUMBER: US/10/533,811
;  CURRENT FILING DATE:  2005-04-29
;  PRIOR APPLICATION NUMBER: US 60/422,303
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: PCT/US2003/034453
;  PRIOR FILING DATE: 2003-10-29
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Lutzomyia longipalpis
US-10-533-811-31

  Query Match             7.4%;  Score 93.5;  DB 6;  Length 350;
  Best Local Similarity   21.4%;  Pred. No. 0.16;
  Matches   41;  Conservative   39;  Mismatches   73;  Indels   39;  Gaps    8;

Qy          4 NSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENS 63
              :| :|   ::| : | |  :|:    || |    | : : :| :::|:     :  || |
Db        180 SSQLLSSPMVSTNKTKEFIRNEIQKVRKVRNFVQETLQKIRDISAAIAKKVKSSECLSNL 239

Qy         64 T----CDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG--VTSKVFLAIRRCSTF 117
              |     :||:  : : |          ||  : :    :  |  : : : : :::| |
Db        240 TDIKGLVSDGINCLKEKF--------NDGKRIILQLYNNLLKGLKIPNDLMVELKKCDTN 291

Qy        118 Q-----RMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNR------YYNRLVRS 166
              |     |:|      || |    : |       | : || |  |  |      |:: :
Db        292 QNNTLGRII------CYF-LTPLQLEK-------EQILLPVEFIKRILELTHYFSTMKED 337

Qy        167 LLECDEDTVSTI 178
              |: |   |:::|
Db        338 LINCGITTIASI 349


RESULT 4
US-10-793-626-2460
; Sequence 2460, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2460
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-2460

  Query Match             6.7%;  Score 85.5;  DB 6;  Length 311;
  Best Local Similarity   25.6%;  Pred. No. 0.83;
  Matches   42;  Conservative   21;  Mismatches   70;  Indels   31;  Gaps    6;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMY------------------DICK 75
              :|:  |  :  | | |::  |     |:   |  | |                  || |
Db         15 SAEKLATEIINLESILELPKGT----EHFVSDLHGEYESFQHVLRNGSGNVRAKINDIFK 70

Qy         76 SFLYSAAKFDTQGKAFV-KESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNV 134
                |      |     :  :| || : |    |   | |   :| ||:| ::   | ||
Db         71 DKLSQQEINDLAALVYYPEEKLKLVKNNFDSIGTLNIWYITTIQRLI-DLITYCSSKYTR 129

Qy        135 CSIAKRNPE----AITEVVQLPNHFSNR--YYNRLVRSLLECDE 172
              : |  ||     | |::   | | |:  ||  ||  ::| ::
Db        130 SKLRKALPEQYVYYIIEELLYKSNEFHNKKPYYETLVNQIIELEQ 173


RESULT 5
US-10-793-626-792
; Sequence 792, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 792
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-792

  Query Match             6.5%;  Score 83;  DB 6;  Length 319;
  Best Local Similarity   19.5%;  Pred. No. 1.5;
```

```
  Matches   52;  Conservative   49;  Mismatches   97;  Indels   68;  Gaps   13;

Qy          5 SAVLLVL-VISASAT-----HEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFA 58
              ||: | | : ::: |     : | ||   ||: |: |  |: |                 |
Db         27 SALTLALYLFNSNVTVYADENTANQNQGTSPKTSQTAPTNNTE---------NTDATAIT 77

Qy         59 CLENSTCDT--DGMYDICKSFLYSAAKFDTQGKAFVKESLK------------------- 97
                :|:  :   |  |::    ||      | ||   :|::::
Db         78 TDQNNNDEEEYDASYEL--PILYVTVWLDDQGN-IIKDAVEDAKTPASERQPVKIPGYQH 134

Qy         98 ---CIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNH 154
                  :::|:|  ::   |: || |  | |  ::  :   |     :| : :    |  |
Db        135 YRTSVSDGITKFIY---RKISTAQSPIVENNQQDNNTNKVVETTNQNKDEVNGKEQ--NQ 189

Qy        155 FSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRR 214
               :    |  : :  | ||||  |::    ||   :  :              |: |  ::
Db        190 ANTSVTNTQI-TKNEKDEDT-KTLKKDKDEKESKDTKT-------------PKKDKEKK 233

Qy        215 RTNEP-----QKLKVLLRNLRGEEDS 235
                |     :|  |: :: : |:|:
Db        234 DIKTPKKDREEKKPVIPKSGKDEKDT 259


RESULT 6
US-10-793-626-2008
; Sequence 2008, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2008
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-2008

  Query Match             6.5%;  Score 83;  DB 6;  Length 319;
  Best Local Similarity   19.5%;  Pred. No. 1.5;
  Matches   52;  Conservative   49;  Mismatches   97;  Indels   68;  Gaps   13;

Qy          5 SAVLLVL-VISASAT-----HEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFA 58
              ||: | | : ::: |     : | ||   ||: |: |  |: |                 |
Db         27 SALTLALYLFNSNVTVYADENTANQNQGTSPKTSQTAPTNNTE---------NTDATAIT 77

Qy         59 CLENSTCDT--DGMYDICKSFLYSAAKFDTQGKAFVKESLK------------------- 97
                :|:  :   |  |::    ||      | ||   :|::::
Db         78 TDQNNNDEEEYDASYEL--PILYVTVWLDDQGN-IIKDAVEDAKTPASERQPVKIPGYQH 134

Qy         98 ---CIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNH 154
                  :::|:|  ::   |: || |  | |  ::  :   |     :| : :    |  |
Db        135 YRTSVSDGITKFIY---RKISTAQSPIVENNQQDNNTNKVVETTNQNKDEVNGKEQ--NQ 189

Qy        155 FSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRR 214
               :    |  : :  | ||||  |::    ||   :  :              |: |  ::
Db        190 ANTSVTNTQI-TKNEKDEDT-KTLKKDKDEKESKDTKT-------------PKKDKEKK 233

Qy        215 RTNEP-----QKLKVLLRNLRGEEDS 235
                |     :|  |: :: : |:|:
Db        234 DIKTPKKDREEKKPVIPKSGKDEKDT 259


RESULT 7
US-11-096-568A-27671
; Sequence 27671, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27671
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(344)
;   OTHER INFORMATION: Ceres Seq. ID no. 1824213
US-11-096-568A-27671

  Query Match             6.5%;  Score 83;  DB 7;  Length 344;
  Best Local Similarity   22.3%;  Pred. No. 1.7;
  Matches   45;  Conservative   27;  Mismatches   76;  Indels   54;  Gaps    9;

Qy          8 LLVLVISASATHEAEQNDSVSPRKSRVAAQN---------SAEVVRCLNSALQVGCGAFA 58
              |  :  : ||    :||: |:|   |:|  |          |:    :| | :|    |
Db         64 LYEIFTALSAASSEKQNEPVAPSSLRIALSNLYPDSSFFQEAQ----MNDASEVLAVIFD 119

Qy         59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQ 118
              ||  |   :  : |:  |        :|   :         |||:              | |
Db        120 CLHRSFAQSSSVSDVDSSDSNCTGSWDCANRT-------CIAH-------------SLFG 159

Qy        119 RMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTI 178
              | | |  |||     | :  |:         ::  : | |   : |    : | |::
Db        160 MDIFE-QLNCYS----CGLESRH-------LKYTSFFHNINASALRTMKVTCAENSF--- 204

Qy        179 RDSLMEKIGPNMASLFHILQTD 200
               | |:     |:  : | |  |
Db        205 -DELL-----NLVEMNHQLACD 220


RESULT 8
US-11-096-568A-27670
; Sequence 27670, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27670
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(365)
;   OTHER INFORMATION: Ceres Seq. ID no. 1824212
US-11-096-568A-27670

  Query Match             6.5%;  Score 83;  DB 7;  Length 365;
  Best Local Similarity   22.3%;  Pred. No. 1.8;
  Matches   45;  Conservative   27;  Mismatches   76;  Indels   54;  Gaps    9;

Qy          8 LLVLVISASATHEAEQNDSVSPRKSRVAAQN---------SAEVVRCLNSALQVGCGAFA 58
              |  :  : ||    :||: |:|   |:|  |          |:    :| | :|    |
Db         85 LYEIFTALSAASSEKQNEPVAPSSLRIALSNLYPDSSFFQEAQ----MNDASEVLAVIFD 140

Qy         59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQ 118
              ||  |   :  : |:  |        :|   :         |||:              | |
```

```
Db        141 CLHRSFAQSSSVSDVDSSDSNCTGSWDCANRT-------CIAH------------SLFG 180

Qy        119 RMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTI 178
                | | |  |||    | :  |:       ::  : | |   : |    : | |::
Db        181 MDIFE-QLNCYS----CGLESRH-------LKYTSFFHNINASALRTMKVTCAENSF--- 225

Qy        179 RDSLMEKIGPNMASLFHILQTD 200
               | |:      |:  : | | |
Db        226 -DELL-----NLVEMNHQLACD 241


RESULT 9
US-10-793-626-44
; Sequence 44, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-44

  Query Match             6.5%;  Score 83;  DB 6;  Length 398;
  Best Local Similarity   22.6%;  Pred. No. 2;
  Matches   44;  Conservative   32;  Mismatches   57;  Indels   62;  Gaps   11;

Qy         57 FACLENSTCDTD-----GMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAI 111
              |   | :| :||     |:||: :||     |  |:||:| : :::     : |:  :|
Db        247 FIKFEEATIETDHTSKQGLYDVIQSF---KDKVRTEGKSFYRLNVR-----INSEDIIAP 298

Qy        112 RRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECD 171
              :     : || | :|                                | |   :   |    :: |
Db        299 QDLIQLKEMITEFEEN----------------------ENQFV--FIEDLNLQYVQND 332

Qy        172 EDTVSTIRDSLMEKIGPNM---ASLFHILQTDHCAQTHPRA-----DFNR----RRTNEP 219
              |  :       :::  | :   ||||    ||     :|||     |:|         |
Db        333 EMPI-------VKEFSPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 383

Qy        220 QKLKVLLRNLRGEED 234
              ::|  |   :|||::
Db        384 ERL--LKDEMRGEQN 396


RESULT 10
US-10-793-626-1498
; Sequence 1498, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-1498

  Query Match             6.5%;  Score 83;  DB 6;  Length 398;
  Best Local Similarity   22.6%;  Pred. No. 2;
  Matches   44;  Conservative   32;  Mismatches   57;  Indels   62;  Gaps   11;

Qy         57 FACLENSTCDTD-----GMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAI 111
              |   | :| :||     |:||: :||     |  |:||:| : :::     : |:  :|
Db        247 FIKFEEATIETDHTSKQGLYDVIQSF---KDKVRTEGKSFYRLNVR-----INSEDIIAP 298

Qy        112 RRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECD 171
              :     : || | :|                                | |   :   |    :: |
Db        299 QDLIQLKEMITEFEEN----------------------ENQFV--FIEDLNLQYVQND 332

Qy        172 EDTVSTIRDSLMEKIGPNM---ASLFHILQTDHCAQTHPRA-----DFNR----RRTNEP 219
              |  :       :::  | :   ||||    ||     :|||     |:|         |
Db        333 EMPI-------VKEFSPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 383

Qy        220 QKLKVLLRNLRGEED 234
              ::|  |   :|||::
Db        384 ERL--LKDEMRGEQN 396


RESULT 11
US-11-096-568A-32051
; Sequence 32051, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32051
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1724)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592046
US-11-096-568A-32051

  Query Match             6.5%;  Score 82.5;  DB 7;  Length 1724;
  Best Local Similarity   24.4%;  Pred. No. 16;
  Matches   49;  Conservative   24;  Mismatches   55;  Indels   73;  Gaps   11;

Qy         66 DTDGMYDICKSFLYSAA---KFDTQGK------AFVKESLKCI----------ANGVTSK 106
              | :|  ||  |  : ||   | ||           :||  :|||             ||  |
Db        360 DEEGWLDIITSLSWEAATLLKPDTSKSGGMDPGGYVK--VKCIPCGRRSESMVVKGVVCK 417

Qy        107 VFLAIRRCST--------------FQRMIAEV--------QEECYSKLNVCSIAKRNPE 143
                :| || ::              :||:  ::        ||  : |: |  |   ||:
Db        418 KNVAHRRMTSKIEKPRLLILGGALEYQRISNQLSSFDTLLQQEMDHLKMAVAKIDSHNPD 477

Qy        144 AITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKI----------------G 187
               |  | :  : |:  |        ||  |   |  |: ||:|:|
Db        478 -ILLVEKSVSRFAQEY-------LLAKDISLVLNIKRSLLERISRCTGAQIVPSIDQLTS 529

Qy        188 PNM--ASLFHILQTDHCAQTH 206
              | :    |||:   :   :||
Db        530 PKLGYCDLFHV---EKFVETH 547


RESULT 12
US-11-096-568A-32050
; Sequence 32050, Application US/11096568A
; Publication No. US20060048240A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32050
;   LENGTH: 1730
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1730)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592045
US-11-096-568A-32050

  Query Match             6.5%;  Score 82.5;  DB 7;  Length 1730;
  Best Local Similarity   24.4%;  Pred. No. 16;
  Matches   49;  Conservative   24;  Mismatches   55;  Indels   73;  Gaps   11;

Qy         66 DTDGMYDICKSFLYSAA---KFDTQGK------AFVKESLKCI----------ANGVTSK 106
              | :|  ||  |  : ||   | ||          :||  :|||            ||  |
Db        366 DEEGWLDIITSLSWEAATLLKPDTSKSGGMDPGGYVK--VKCIPCGRRSESMVVKGVVCK 423

Qy        107 VFLAIRRCST--------------FQRMIAEV--------QEECYSKLNVCSIAKRNPE 143
                :| || ::              :||:  ::        ||  : |: |  |   ||:
Db        424 KNVAHRRMTSKIEKPRLLILGGALEYQRISNQLSSFDTLLQQEMDHLKMAVAKIDSHNPD 483

Qy        144 AITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKI----------------G 187
              |  | :  : |:  |       ||  |   |  |: ||:|:|
Db        484 -ILLVEKSVSRFAQEY-------LLAKDISLVLNIKRSLLERISRCTGAQIVPSIDQLTS 535

Qy        188 PNM--ASLFHILQTDHCAQTH 206
              | :    |||:   :   :||
Db        536 PKLGYCDLFHV---EKFVETH 553


RESULT 13
US-11-096-568A-32049
; Sequence 32049, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32049
;   LENGTH: 1757
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1757)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592044
US-11-096-568A-32049

  Query Match             6.5%;  Score 82.5;  DB 7;  Length 1757;
  Best Local Similarity   24.4%;  Pred. No. 16;
  Matches   49;  Conservative   24;  Mismatches   55;  Indels   73;  Gaps   11;

Qy         66 DTDGMYDICKSFLYSAA---KFDTQGK------AFVKESLKCI----------ANGVTSK 106
              | :|  ||  |  : ||   | ||          :||  :|||            ||  |
Db        393 DEEGWLDIITSLSWEAATLLKPDTSKSGGMDPGGYVK--VKCIPCGRRSESMVVKGVVCK 450

Qy        107 VFLAIRRCST--------------FQRMIAEV--------QEECYSKLNVCSIAKRNPE 143
                :| || ::              :||:  ::        ||  : |: |  |   ||:
Db        451 KNVAHRRMTSKIEKPRLLILGGALEYQRISNQLSSFDTLLQQEMDHLKMAVAKIDSHNPD 510

Qy        144 AITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKI----------------G 187
              |  | :  : |:  |       ||  |   |  |: ||:|:|
Db        511 -ILLVEKSVSRFAQEY-------LLAKDISLVLNIKRSLLERISRCTGAQIVPSIDQLTS 562

Qy        188 PNM--ASLFHILQTDHCAQTH 206
              | :    |||:   :   :||
Db        563 PKLGYCDLFHV---EKFVETH 580


RESULT 14
US-11-096-568A-27511
; Sequence 27511, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27511
;   LENGTH: 2535
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2535)
;   OTHER INFORMATION: Ceres Seq. ID no. 1819121
US-11-096-568A-27511

  Query Match             6.5%;  Score 82.5;  DB 7;  Length 2535;
  Best Local Similarity   15.9%;  Pred. No. 27;
  Matches   53;  Conservative   58;  Mismatches   91;  Indels  131;  Gaps   13;

Qy         12 VISASATHEAEQND---SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTD 68
              |::  :|||:  :   ::   : :: :  : | |: |                    :|
Db         17 VMAFRPSHEAKLRELLHNICLHEIKLCSDAAKEFVKLLKG----------------ETG 59

Qy         69 GMYDICKSFLYSAAKF----------DTQGKAFVKESLKCIAN---GVTSKVFLAIRRC 114
              |  |: : :  |:  |          : || :::   :: | : |      :  |
Db         60 G--DLLRLYFQSSPNFAELLEAWKLRHEKQGLSYIFSLIQTILSHPEGKDRSTDIG-RAI 116

Qy        115 STFQRMIAEVQ-EECYSKLN-------------VCSIAKRNPEAITEVV---------- 149
                | |:: | : :: | :||             : || :| |   :|:
Db        117 DQFGRLLVEEKLDDIYKELNSKEGKQQSAALSLLASIVRRGPGMASEIAKKFDFKGFAKL 176

Qy        150 ---------QLPNHFSNR-------------------------YYNRLVRSLLECDEDT 174
                      ::  | : :                         |::::  | : |:||
Db        177 AEYNTQGTEKVKKHSTRKAFVGFAISFLEVGKPGLLSSVLNKKEMYSKVLPGLGKDDDDT 236

Qy        175 VSTIRDSLMEK-------IGPNMAS-LFHILQTDHCAQTHPR------------------ 208
              |:::  :| :|       | | : | || |:   | |    |
Db        237 VASVLSTLKDKILVEESLISPGLRSVLFGIVTLKHLASISAREDAGIVNELAHDVLVKVC 296

Qy        209 --------ADFNRRRTNEPQKLKVLLRNLRGEE 233
                       |  |:      :| :|:: ||  |
Db        297 TDPSNGLMPDAKRKLRGNSDRLLMLMKGLRAAE 329


RESULT 15
US-11-096-568A-27512
; Sequence 27512, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27512
```

```
;   LENGTH: 2518
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2518)
;   OTHER INFORMATION: Ceres Seq. ID no. 1819122
US-11-096-568A-27512

  Query Match             6.4%;  Score 81.5;  DB 7;  Length 2518;
  Best Local Similarity   19.4%;  Pred. No. 33;
  Matches   49;  Conservative   38;  Mismatches   80;  Indels   85;  Gaps   10;

Qy          20 EAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLY 79
               | : :|       |:   | ||  :  | | :: | |  :             :| | | :
Db         108 EEKLDDIYKELNSKEGKQQSA-ALSLLASIVRRGPGMAS------------EIAKKFDF 153

Qy          80 SA----AKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVC 135
                    |:::|||   ||:          | | |:                        ::
Db         154 KGFAKLAEYNTQGTEKVKKH-------STRKAFVGF------------------AISFL 187

Qy         136 SIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEK-------IGP 188
                : |  |  :: |:          |::::  | : |:|||:::  :| :|       | |
Db         188 EVGK--PGLLSSVLN-----KKEMYSKVLPGLGKDDDDTVASVLSTLKDKILVEESLISP 240

Qy         189 NMAS-LFHILQTDHCAQTHPR-------------------------ADFNRRRTNEPQK 221
                : | || |:   | |    |                        |  |:      :
Db         241 GLRSVLFGIVTLKHLASISAREDAGIVNELAHDVLVKVCTDPSNGLMPDAKRKLRGNSDR 300

Qy         222 LKVLLRNLRGEE 233
               | :|:: ||  |
Db         301 LLMLMKGLRAAE 312


Search completed: April  4, 2006, 14:30:18
Job time : 26 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:07:08 ; Search time 189 Seconds
(without alignments)
574.215 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	2	AAR84522	Aar84522 Stannioca
2	1268	100.0	247	3	AAB23264	Aab23264 Human sta
3	1268	100.0	247	3	AAY55750	Aay55750 Human sta
4	1268	100.0	247	3	AAY57166	Aay57166 Human cor
5	1268	100.0	247	3	AAY92901	Aay92901 Human sta
6	1268	100.0	247	4	AAB62473	Aab62473 Human sta
7	1268	100.0	247	4	AAB62690	Aab62690 Lng108, a
8	1268	100.0	247	5	ABB06259	Abb06259 Human sta
9	1268	100.0	247	6	ABP97748	Abp97748 Amino aci
10	1268	100.0	247	6	ABR47600	Abr47600 Breast ca
11	1268	100.0	247	6	ABG72290	Abg72290 Human Cor
12	1268	100.0	247	7	ADD48082	Add48082 Human Pro
13	1268	100.0	247	7	ADI30575	Adi30575 Human sta
14	1268	100.0	247	7	ABO84399	Abo84399 Human sta
15	1268	100.0	247	8	ADQ21382	Adq21382 Human sof
16	1268	100.0	247	8	ADR87637	Adr87637 Human Sta
17	1268	100.0	247	9	AEB08112	Aeb08112 Human sta
18	1268	100.0	255	9	AEB54713	Aeb54713 Human sta
19	1234	97.3	247	9	AEB08116	Aeb08116 Mouse sta
20	1231	97.1	247	7	ADD48080	Add48080 Rat Prote
21	937	73.9	276	3	AAB56848	Aab56848 Human pro
22	680.5	53.7	261	1	AAP82968	Aap82968 Corpuscle
23	662.5	52.2	256	4	AAB62474	Aab62474 Coho salm
24	628	49.5	170	3	AAY55749	Aay55749 A. austra
25	628	49.5	170	7	ADI30574	Adi30574 Australia
26	358	28.2	70	4	AAM18134	Aam18134 Peptide #
27	358	28.2	70	4	ABB37166	Abb37166 Peptide #
28	358	28.2	70	4	AAM30637	Aam30637 Peptide #
29	358	28.2	70	4	ABB31928	Abb31928 Peptide #
30	358	28.2	70	4	ABB22472	Abb22472 Protein #
31	358	28.2	70	4	AAM70300	Aam70300 Human bon
32	358	28.2	70	4	AAM57878	Aam57878 Human bra
33	358	28.2	70	4	ABG52000	Abg52000 Human liv
34	358	28.2	70	4	AAM05763	Aam05763 Peptide #
35	358	28.2	70	5	ABG39940	Abg39940 Human pep
36	354.5	28.0	296	3	AAY67926	Aay67926 Mouse sta
37	354.5	28.0	296	4	AAB61623	Aab61623 Murine st
38	354.5	28.0	296	9	AEB08118	Aeb08118 Mouse sta
39	354	27.9	293	2	AAY41255	Aay41255 Adipogene
40	354	27.9	293	3	AAB26872	Aab26872 Human adi
41	354	27.9	293	4	AAB93965	Aab93965 Human pro
42	354	27.9	302	3	AAY67925	Aay67925 Human sta
43	354	27.9	302	4	AAB98971	Aab98971 Human adi
44	354	27.9	302	4	AAB61621	Aab61621 Human sta
45	354	27.9	302	4	AAB31797	Aab31797 Amino aci

ALIGNMENTS

RESULT 1
AAR84522
ID AAR84522 standard; protein; 247 AA.
XX
AC AAR84522;
XX
DT 19-APR-1996 (first entry)
XX
DE Stanniocalcin from Corpuscles of Stannius.
XX
KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .33
FT /label= prepro_region
FT Protein 34. .247
FT /label= mature_stanniocalcin
XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US005136.
XX
PR 08-MAR-1994; 94US-00208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen H, Adams MD;
XX
DR WPI; 1995-328227/42.
DR N-PSDB; AAT02438.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.
XX
PS Claim 14; Fig 1; 41pp; English.
XX
CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
CC used for the treatment of e.g. electrolyte disorders which lead to renal,
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease
XX

```
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 2
AAB23264
ID   AAB23264 standard; protein; 247 AA.
XX
AC   AAB23264;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human stanniocalcin.
XX
KW   Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW   mineral metabolism regulator; prophylaxis; therapy.
XX
OS   Homo sapiens.
XX
PN   JP2000229880-A.
XX
PD   22-AUG-2000.
XX
PF   10-FEB-1999;   99JP-00033262.
XX
PR   10-FEB-1999;   99JP-00033262.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
DR   WPI; 2000-605236/58.
DR   N-PSDB; AAA97594.
XX
PT   An osteogenesis promotor useful in the prevention and/or treatment of
PT   bone diseases such as osteoporosis.
XX
PS   Example 1; Page 5-6; 6pp; Japanese.
XX
CC   The invention relates to a novel osteogenesis-promoting composition which
CC   contains stanniocalcin (STC) as the active component. Stanniocalcin is a
CC   possible regulator of mineral metabolism. The composition is useful as a
CC   prophylactic and/or therapeutic agent for bone diseases such as
CC   osteoporosis. The present sequence represents human stanniocalcin which
CC   was used in an exemplification of the invention
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 3;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 3
AAY55750
ID   AAY55750 standard; protein; 247 AA.
XX
AC   AAY55750;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Human stanniocalcin polypeptide.
XX
KW   Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
KW   anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW   parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW   electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW   Paget's disease; hypercalcemia.
XX
OS   Homo sapiens.
XX
PN   US5994103-A.
XX
PD   30-NOV-1999.
XX
PF   02-JUN-1995;   95US-00460529.
XX
PR   10-NOV-1994;   94WO-US013206.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Fleischmann RD,  Olsen HS;
XX
DR   WPI; 2000-038260/03.
XX
PT   Isolated nucleic acids encoding human stanniocalcin-alpha useful for
PT   treating electrolyte disorders which lead to renal, bone and heart
PT   diseases, osteoporosis and Paget's disease.
XX
PS   Disclosure; Fig 3; 21pp; English.
XX
CC   The invention provides a human stanniocalcin-alpha polypeptide (also
CC   called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
CC   hypercalcemic glycoprotein hormone produced by the corpuscles of
CC   stannius. It has a similar reported biological activity to that of
CC   parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC   in mammals. They exert hypercalcemic activity due to stimulation of bone
CC   reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC   at low doses it increases bone formation and at high doses it increases
CC   bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC   of it (under different circumstances) may be used to treat osteoporosis.
CC   The DNA may be used to produce human stanniocalcin-alpha according to
CC   standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC   be produced either in vitro in a fermentation culture or in vivo as part
CC   of a gene therapy protocol, and may be used to treat electrolyte
```

```
CC   disorders which lead to renal, bone and heart diseases. Due to the
CC   biphasic nature of stanniocalcin-alpha it may be used to treat
CC   osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC   polypeptides may be used as antigens in the production of antibodies to
CC   stanniocalcin-alpha and to assay for agonists and antagonists of its
CC   activity. The antibodies and antagonists may be used to inhibit the
CC   activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC   hypercalcemia. The present sequence represents a human stanniocalcin
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 3;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 4
AAY57166
ID   AAY57166 standard; protein; 247 AA.
XX
AC   AAY57166;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Human corpuscles of stanius polypeptide.
XX
KW   Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW   therapeutic; bone; heart disease; hypocalcemia; osteoperosis.
XX
OS   Homo sapiens.
XX
PN   US5994301-A.
XX
PD   30-NOV-1999.
XX
PF   28-APR-1995;   95US-00431117.
XX
PR   08-MAR-1994;   94US-00208005.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Adams MD,  Olsen HS;
XX
DR   WPI; 2000-038269/03.
DR   N-PSDB; AAZ39520.
XX
PT   Human corpuscles of stanius polypeptides used to inhibit calcium uptake.
XX
PS   Claim 4; Fig 1A-B; 23pp; English.
XX
CC   This represents a human corpuscles of stanius polypeptide, having a
CC   calcium uptake inhibitory activity. The cDNA is deposited under the
CC   accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC   method for the treatment of a patient having need to inhibit uptake of
CC   calcium. The method is also used for the therapeutic treatment of renal,
CC   bone, and heart diseases, and the antagonist (may be an antibody) may be
CC   used for treating hypocalcemia., and osteoperosis
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 3;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 5
AAY92901
ID   AAY92901 standard; protein; 247 AA.
XX
AC   AAY92901;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human stanniocalcin protein.
XX
KW   PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW   adipocyte; obesity; diabetes; hypertension; heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200016795-A1.
XX
PD   30-MAR-2000.
XX
PF   17-SEP-1999;   99WO-JP005080.
XX
PR   17-SEP-1998;   98JP-00263004.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Goto M,  Tomoyasu A,  Yamaguchi K,  Kinosaki M,  Nakagawa N;
XX
DR   WPI; 2000-283445/24.
DR   N-PSDB; AAA11145.
XX
PT   Treating or preventing obesity, which is a risk factor for diabetes,
PT   hypertension and heart disease, comprises administering an agent
PT   containing stanniocalcin.
XX
PS   Example 1; Page 16; 19pp; Japanese.
XX
CC   This sequence represents the human stanniocalcin protein. Stanniocalcin
CC   is an inhibitor of the differentiation and maturation of adipocytes. The
CC   protein is used for preventing and treating obesity which is a risk
CC   factor for diabetes, hypertension, and heart disease. The coding sequence
CC   was isolated from IMR-90 cells
```

```
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 3;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 6
AAB62473
ID   AAB62473 standard; protein; 247 AA.
XX
AC   AAB62473;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Human stanniocalcin (STC) protein.
XX
KW   Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW   antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW   nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW   antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW   antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW   hemostatic; thrombolytic.
XX
OS   Homo sapiens.
XX
PN   WO200130969-A2.
XX
PD   03-MAY-2001.
XX
PF   20-OCT-2000; 2000WO-US029432.
XX
PR   27-OCT-1999;   99US-0161740P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (UYHE-) UNIV HELSINKI.
XX
PI   Olsen HS,  Zhang K,  Lindsberg P,  Tatlisumak T,  Kaste M;
PI   Andersson LC;
XX
DR   WPI; 2001-308626/32.
DR   N-PSDB; AAF83297.
XX
PT   Novel composition useful for treating or protecting neural cells, for
PT   treating Addison's disease, organ rejection, hyperproliferative disorder,
PT   cancer, AIDS, multiple sclerosis, comprises stanniocalcin polypeptide.
XX
PS   Claim 1; Fig 1A-C; 253pp; English.
XX
CC   The invention relates to a human stanniocalcin (STC) polypeptide. A
CC   pharmaceutical composition comprising the STC is useful for treating a
CC   patient in need of increased levels of STC activity. STC and its
CC   modulators are useful for treating disorders or abnormalities of nervous
CC   system, cerebrovascular diseases, dementia, encephalitis, central nervous
CC   system infections or neoplasms, demyelinating diseases,
CC   encephalomyelitis, spinal cord diseases, mental retardation such as
CC   Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC   muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC   immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC   arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC   Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC   lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC   reactions and conditions such as asthma, for treating and/or preventing
CC   organ rejection or graft-versus-host disease, hyperproliferative diseases
CC   such as purpura, Gaucher's disease, cardiovascular disorders such as
CC   arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC   disorders with neovascularization. The composition can be used to treat
CC   hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC   wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC   Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC   Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC   or detecting infectious agents. The present sequence represents the human
CC   STC polypeptide
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 7
AAB62690
ID   AAB62690 standard; protein; 247 AA.
XX
AC   AAB62690;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Lng108, a diagnostic marker for cancer.
XX
KW   Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
XX
OS   Homo sapiens.
XX
PN   WO200132209-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030482.
XX
PR   04-NOV-1999;   99US-0163444P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
```

PI Recipon H, Macina RA, Chen S, Sun Y;
XX
DR WPI; 2001-316386/33.
DR N-PSDB; AAF83823.
XX
PT Novel assay for diagnosing and monitoring cancer, involves determining
PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT comparing with control.
XX
PS Disclosure; Page 33-34; 36pp; English.
XX
CC The invention relates to diagnosing the presence of cancer or diagnosing
CC metastases of cancer in a patient that involves determining levels of
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC comparing the determined levels with levels of Lng108 a normal human
CC control. The method is useful for diagnosing the presence of cancer,
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC monitoring a change in stage of the cancer, in a patient. A therapeutic
CC agent which is an antibody labeled with paramagnetic ions or a
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC cancer in a patient. A molecule which downregulates the expression or
CC activity of Lng108, is useful for treating cancer in a patient. Lng108
CC protein is useful for inducing an immune response against a target cell
CC expressing Lng108. The present sequence represents the human Lng108
CC polypeptide
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 8
ABB06259
ID ABB06259 standard; protein; 247 AA.
XX
AC ABB06259;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human staniocalcin 1 protein.
XX
KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.
XX
OS Homo sapiens.
XX
PN WO200204013-A1.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-JP005962.
XX
PR 11-JUL-2000; 2000JP-00209926.
XX
PA (BMLB-) BML INC.
XX
PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;
XX
DR WPI; 2002-164600/21.
DR N-PSDB; ABL40225.
XX
PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I.
XX
PS Claim 2; Fig 1; 24pp; Japanese.
XX
CC The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human staniocalcin 1
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 9
ABP97748
ID ABP97748 standard; protein; 247 AA.
XX
AC ABP97748;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human STC1 polypeptide.
XX
KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mig-6; SSR4;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO2003010205-A1.
XX

PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-US023786.
XX
PR 26-JUL-2001; 2001US-0307600P.
PR 24-JUL-2002; 2002US-00201642.
XX
PA (UYDU-) UNIV DUKE MEDICAL CENT.
XX
PI Riggins GJ, Lal A;
XX
DR WPI; 2003-239423/23.
DR N-PSDB; ABZ77288.
XX
PT Inhibiting angiogenesis for treating wound healing, retinopathy,
PT ischemia, inflammation, microvasculopathy, bone healing, skin
PT inflammation or follicular development by providing to a subject an
PT antisense polynucleotide.
XX
PS Claim 4; Page 61; 66pp; English.
XX
CC The present sequence is a human STC1 polypeptide. It is used in the
CC method of the invention. The specification describes a method modulating
CC angiogenesis associated with wound healing, retinopathy, ischemia,
CC inflammation, microvasculopathy, bone healing, skin inflammation or
CC follicular development. The method comprises providing to a subject HOG3,
CC HOG8, HOG18, CA9, HXB, IGFBP5, HFARP, STC1, mig-6 or SSR4. The methods,
CC antisense polynucleotides, polypeptides and antibodies are useful for
CC treating wound healing, retinopathy, ischemia, inflammation,
CC microvasculopathy, bone healing, skin inflammation or follicular
CC development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 10
ABR47600
ID ABR47600 standard; protein; 247 AA.
XX
AC ABR47600;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:441.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.

XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR N-PSDB; ACC50301.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 441; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 11
ABG72290
ID ABG72290 standard; protein; 247 AA.

XX
AC ABG72290;
XX
DT 14-MAR-2003 (first entry)
XX
DE Human Corpuscles of Stannius protein.
XX
KW Human; Corpuscles of Stannius protein; calcium uptake inhibitor;
KW renal excretion of phosphate; electrolyte disorder; renal disease;
KW bone disease; heart disease; arterial hypertension; bone resorption;
KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
KW hypervitaminosis D; tumour; serum calcium level; sarcoidosis;
KW hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;
KW GI calcium absorption; stanniocalcin; osteopathic; cytostatic;
KW hypotensive.
XX
OS Homo sapiens.
XX
PN US2002146791-A1.
XX
PD 10-OCT-2002.
XX
PF 05-APR-2002; 2002US-00116051.
XX
PR 08-MAR-1994; 94US-00208005.
PR 28-APR-1995; 95US-00431117.
PR 17-MAY-1999; 99US-00312610.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen HS, Adams MD;
XX
DR WPI; 2003-147579/14.
DR N-PSDB; ABX15152.
XX
PT Isolated polynucleotide for encoding polypeptides used to diagnose and
PT treat electrolyte disorders leading to renal disease, e.g. Paget's
PT disease, hypercalcemia and sarcoidosis.
XX
PS Claim 13; Fig 1; 26pp; English.
XX
CC The present invention relates to the isolation of human Corpuscles of
CC Stannius protein, and the polynucleotide sequence encoding it. Human
CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal
CC excretion of phosphate. The polynucleotide sequence is useful for
CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in
CC the treatment of electrolyte disorders that lead to renal, bone or heart
CC disease, such as arterial hypertension, disorders due to elevated bone
CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia
CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum
CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal
CC insufficiency, loss of serum albumin secondary to renal diseases, or
CC excessive GI calcium absorption and elevated concentration of plasma
CC proteins. The encoded polypeptide exhibits a high degree of homology to
CC Stanniocalcin from Anguilla australis and from Oncorhynchus kisutch. The
CC present sequence represents human corpuscles of stannius protein
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 12
ADD48082
ID ADD48082 standard; protein; 247 AA.
XX
AC ADD48082;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P52823, SEQ ID NO 13779.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P52823.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

```
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 13
ADI30575
ID   ADI30575 standard; protein; 247 AA.
XX
AC   ADI30575;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human stannicoalcin protein.
XX
KW   human; stanniocalcin-alpha; electrolyte imbalance; hypertension;
KW   hyperglycaemia; migraine; renal disease; heart disease; bone disease;
KW   osteoporosis; hypoglycaemia; Paget's disease.
XX
OS   Homo sapiens.
XX
PN   US2003181663-A1.
XX
PD   25-SEP-2003.
XX
PF   18-APR-2003; 2003US-00418226.
XX
PR   10-NOV-1994;   94WO-US013206.
PR   02-JUN-1995;   95US-00460529.
PR   28-JUL-1999;   99US-00361736.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Olsen HS,  Fleischmann RD;
XX
DR   WPI; 2003-852260/79.
XX
PT   New human stanniocalcin-alpha polypeptide, useful in regulating
PT   electrolyte imbalances, or for diagnosing and treating a disease
PT   associated with mutated forms of stanniocalcin-alpha sequences, e.g.
PT   renal disease or osteoporosis.
XX
PS   Disclosure; SEQ ID NO 10; 22pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of a human
CC   stanniocalcin-alpha protein. The DNA and protein sequences of the
CC   invention are useful for regulating electrolyte imbalances to treat
CC   hypertension, hyperglycaemia or migraine. The DNA and protein sequences
CC   are also useful in diagnosing and treating a disease associated with
CC   mutated forms of stannicoalcin-alpha sequences, such as: renal disease,
CC   heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC   sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC   present amino acid sequence represents a human stannicoalcin protein.
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 14
ABO84399
ID   ABO84399 standard; protein; 247 AA.
XX
AC   ABO84399;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human stanniocalcin protein.
XX
KW   Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW   respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW   surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW   analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW   beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW   respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW   emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW   pulmonary transplantation rejection.
XX
OS   Homo sapiens.
XX
PN   WO200285309-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013143.
XX
PR   24-APR-2001; 2001US-0286036P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-093058/08.
DR   N-PSDB; ABD20997.
```

```
XX
PT   Pharmaceutical composition for treating asthma, has antisense
PT   oligonucleotide containing less percentage of adenosine, targeted to
PT   nucleic acids associated with lung airway or lung dysfunction, and
PT   bronchodilating agent.
XX
PS   Claim 15; SEQ ID NO 6; 763pp; English.
XX
CC   This invention describes a novel composition (a) a first active agent,
CC   comprising oligonucleotides, effective for alleviating
CC   bronchoconstriction, respiratory tract inflammation, allergies and
CC   reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC   surfactant depletion or hyposecretion, when administered to a mammal. The
CC   oligonucleotides are derived from a gene encoding or regulating
CC   expression of a target polypeptide associated with lung airway or lung
CC   dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC   The invention also describes a kit, that comprises: (a) a delivery
CC   device, in separate containers, (b) the oligonucleotides, (c)
CC   instructions for adding a carrier and for use of the kit. The composition
CC   of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC   analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC   beta-adrenergic agonist. The composition is useful for preventing or
CC   treating a respiratory, lung or malignant disease. The administered
CC   composition comprises oligo and is administered to reduce the production
CC   or availability, or to increase the degradation of the target mRNA or to
CC   reduce the amount of target polypeptide present in the lungs. The
CC   pulmonary obstruction, and/or bronchoconstriction and/or lung
CC   inflammation, allergies and/or surfactant hypoproduction are associated
CC   with a disease or condition such as pulmonary vasoconstriction,
CC   inflammation, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 15
ADQ21382
ID   ADQ21382 standard; protein; 247 AA.
XX
AC   ADQ21382;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 4202.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 4202; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   protein of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 247 AA;

  Query Match             100.0%;  Score 1268;  DB 8;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-123;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


Search completed: April  4, 2006, 14:10:41
Job time : 193 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:14:54 ; Search time 47 Seconds
(without alignments)
434.487 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	1	US-08-208-005C-2	Sequence 2, Appli
2	1268	100.0	247	1	US-09-038-597A-2	Sequence 2, Appli
3	1268	100.0	247	1	US-08-460-529B-10	Sequence 10, Appl
4	1268	100.0	247	1	US-08-431-117A-2	Sequence 2, Appli
5	1268	100.0	247	2	US-09-361-736B-10	Sequence 10, Appl
6	1268	100.0	247	2	US-09-949-016-6319	Sequence 6319, Ap
7	1268	100.0	247	2	US-09-787-397A-4	Sequence 4, Appli
8	1268	100.0	247	2	US-09-705-500A-3	Sequence 3, Appli
9	1268	100.0	247	2	US-10-418-226-10	Sequence 10, Appl
10	1268	100.0	341	2	US-09-949-016-11426	Sequence 11426, A
11	660.5	52.1	204	1	US-08-208-005C-5	Sequence 5, Appli
12	660.5	52.1	204	1	US-09-038-597A-5	Sequence 5, Appli
13	628	49.5	170	1	US-08-460-529B-9	Sequence 9, Appli
14	628	49.5	170	2	US-09-361-736B-9	Sequence 9, Appli
15	628	49.5	170	2	US-10-418-226-9	Sequence 9, Appli
16	354.5	28.0	296	2	US-08-831-132-14	Sequence 14, Appl
17	354.5	28.0	296	2	US-09-416-150-14	Sequence 14, Appl
18	354	27.9	302	2	US-08-831-132-2	Sequence 2, Appli
19	354	27.9	302	2	US-09-416-150-2	Sequence 2, Appli
20	354	27.9	302	2	US-09-193-881-23	Sequence 23, Appl
21	354	27.9	302	2	US-09-361-736B-12	Sequence 12, Appl
22	354	27.9	302	2	US-10-418-226-12	Sequence 12, Appl
23	354	27.9	346	2	US-09-949-016-10679	Sequence 10679, A
24	351.5	27.7	251	2	US-09-361-736B-2	Sequence 2, Appli
25	351.5	27.7	251	2	US-10-418-226-2	Sequence 2, Appli
26	333.5	26.3	251	1	US-08-460-529B-2	Sequence 2, Appli
27	91	7.2	901	2	US-09-828-062-8	Sequence 8, Appli
28	90	7.1	281	2	US-09-973-278-172	Sequence 172, App
29	90	7.1	281	2	US-09-973-278-277	Sequence 277, App
30	89.5	7.1	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
31	86	6.8	500	2	US-09-198-452A-299	Sequence 299, App
32	86	6.8	500	2	US-09-438-185A-288	Sequence 288, App
33	85.5	6.7	311	2	US-09-710-279-2460	Sequence 2460, Ap
34	85.5	6.7	656	2	US-09-134-001C-4322	Sequence 4322, Ap
35	83.5	6.6	290	2	US-09-655-908-6	Sequence 6, Appli
36	83.5	6.6	290	2	US-09-655-908-8	Sequence 8, Appli
37	83.5	6.6	1027	2	US-09-762-724-8	Sequence 8, Appli
38	83.5	6.6	1029	2	US-09-762-724-6	Sequence 6, Appli
39	83	6.5	319	2	US-09-710-279-792	Sequence 792, App
40	83	6.5	319	2	US-09-710-279-2008	Sequence 2008, Ap
41	83	6.5	398	2	US-09-710-279-44	Sequence 44, Appl
42	83	6.5	398	2	US-09-710-279-1498	Sequence 1498, Ap
43	83	6.5	417	2	US-09-134-001C-3810	Sequence 3810, Ap
44	82	6.5	362	2	US-09-134-001C-4670	Sequence 4670, Ap
45	81	6.4	680	2	US-09-298-924-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-2

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
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RESULT 2
US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-038-597A-2

  Query Match           100.0%;  Score 1268;  DB 1;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-136;
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247
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RESULT 3
US-08-460-529B-10
; Sequence 10, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-460-529B-10

  Query Match           100.0%;  Score 1268;  DB 1;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
                 |||||||
Db        241 RTSHESA 247
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RESULT 4
US-08-431-117A-2
; Sequence 2, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
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RESULT 5
US-09-361-736B-10
; Sequence 10, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247
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RESULT 6
US-09-949-016-6319
; Sequence 6319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6319
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6319

  Query Match             100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 7
US-09-787-397A-4
; Sequence 4, Application US/09787397A
; Patent No. 6815417
; GENERAL INFORMATION:
;  APPLICANT: Goto, Masaaki      Tomoyasu, Akihiro      Yamaguchi, Kyoji
;  APPLICANT:  Kinosaki, Masahiko      Nakagawa, No. 6815417uaki
;  TITLE OF INVENTION: PREVENTIVE AND/OR THERAPEUTIC FOR OBESITY
;  FILE REFERENCE: FJIN-107
;  CURRENT APPLICATION NUMBER: US/09/787,397A
;  CURRENT FILING DATE:  2002-06-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Human
;  PUBLICATION INFORMATION:
;   AUTHORS: Olsen H. S. et al.
;   TITLE: Human stanniocalcin: A possible hormonal regulator of mineral metabolism.
;   JOURNAL: Proc. Natl. Acad. Sci. USA
;   VOLUME: 93
;   ISSUE: 5
;   PAGES: 1792
;   DATE: 1996-03-05
US-09-787-397A-4

  Query Match             100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 8
US-09-705-500A-3
; Sequence 3, Application US/09705500A
; Patent No. 6902890
; GENERAL INFORMATION:
;  APPLICANT: Recipon, Herve
;  APPLICANT:  Macina, Roberto A.
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Sun, Yongming
;  TITLE OF INVENTION: A No. 6902890el Method of Diagnosing, Monitoring, Staging,
;  TITLE OF INVENTION:  Imaging and Treating Cancer
;  FILE REFERENCE: DEX-0087
;  CURRENT APPLICATION NUMBER: US/09/705,500A
;  CURRENT FILING DATE:  2000-11-03
;  PRIOR APPLICATION NUMBER: 60/163,444
;  PRIOR FILING DATE: 1999-11-04
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-705-500A-3

  Query Match             100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 9
US-10-418-226-10
; Sequence 10, Application US/10418226
; Patent No. 6955885
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Stanniocalcin-Alpha
;  FILE REFERENCE: PF143P1D2
;  CURRENT APPLICATION NUMBER: US/10/418,226
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 09/361,736
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: 08/460,529
```

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;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/ US94/13206
;  PRIOR FILING DATE: 1994-11-30
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: human
US-10-418-226-10

  Query Match            100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 10
US-09-949-016-11426
; Sequence 11426, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11426
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11426

  Query Match            100.0%;  Score 1268;  DB 2;  Length 341;
  Best Local Similarity  100.0%;  Pred. No. 4.3e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 154

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 214

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 274

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 334

Qy        241 RTSHESA 247
              |||||||
Db        335 RTSHESA 341


RESULT 11
US-08-208-005C-5
; Sequence 5, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  204 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-208-005C-5

  Query Match            52.1%;  Score 660.5;  DB 1;  Length 204;
  Best Local Similarity  60.8%;  Pred. No. 4.9e-67;
  Matches  118;  Conservative   38;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| |||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190
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Qy        191 ASLFHILQTDHCAQ 204
              :|| :||  || |
Db        191 ETLFQLLQNKHCPQ 204


RESULT 12
US-09-038-597A-5
; Sequence 5, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  204 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-038-597A-5

  Query Match             52.1%;  Score 660.5;  DB 1;  Length 204;
  Best Local Similarity   60.8%;  Pred. No. 4.9e-67;
  Matches  118;  Conservative   38;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQ 204
              :|| :||  || |
Db        191 ETLFQLLQNKHCPQ 204


RESULT 13
US-08-460-529B-9
; Sequence 9, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  170 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-460-529B-9

  Query Match             49.5%;  Score 628;  DB 1;  Length 170;
  Best Local Similarity   66.5%;  Pred. No. 1.9e-63;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||:|||||| |||||:||:||:||||||||::||:|: ||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
              | |:|: | |||| |::||| ||||||  :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


RESULT 14
US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Stanniocalcin-Alpha
;  FILE REFERENCE: PF143P1D1
;  CURRENT APPLICATION NUMBER: US/09/361,736B
;  CURRENT FILING DATE:  1999-07-28
;  PRIOR APPLICATION NUMBER: 08/460,529
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/ US94/13206
;  PRIOR FILING DATE: 1994-11-30
```

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;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Anguilla australis
US-09-361-736B-9

  Query Match             49.5%;  Score 628;  DB 2;  Length 170;
  Best Local Similarity   66.5%;  Pred. No. 1.9e-63;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||:|||||| |||||:||:||:||||||||||::||:|: ||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
              | |:|: | ||||: |::||| ||||||  :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


RESULT 15
US-10-418-226-9
; Sequence 9, Application US/10418226
; Patent No. 6955885
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Stanniocalcin-Alpha
;  FILE REFERENCE: PF143P1D2
;  CURRENT APPLICATION NUMBER: US/10/418,226
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 09/361,736
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: 08/460,529
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/ US94/13206
;  PRIOR FILING DATE: 1994-11-30
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Anguilla australis
US-10-418-226-9

  Query Match             49.5%;  Score 628;  DB 2;  Length 170;
  Best Local Similarity   66.5%;  Pred. No. 1.9e-63;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||:|||||| |||||:||:||:||||||||||::||:|: ||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
              | |:|: | ||||: |::||| ||||||  :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


Search completed: April  4, 2006, 14:16:15
Job time : 48 secs
```

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:07:39 ; Search time 231 Seconds
(without alignments)
754.396 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	1	STC1_HUMAN	P52823 homo sapien
2	1234	97.3	247	1	STC1_MOUSE	O55183 mus musculu
3	1231	97.1	247	1	STC1_RAT	P97574 rattus norv
4	1228	96.8	247	2	Q71UE3_MOUSE	Q71ue3 mus musculu
5	1199	94.6	247	1	STC1_BOVIN	Q9n0t1 bos taurus
6	1192.5	94.0	246	2	Q7TSN9_MOUSE	Q7tsn9 mus musculu
7	873	68.8	251	2	Q5XGL3_XENLA	Q5xgl3 xenopus lae
8	851	67.1	253	2	Q6DFI8_XENLA	Q6dfi8 xenopus lae
9	797	62.9	157	2	Q71UE5_HUMAN	Q71ue5 homo sapien
10	779.5	61.5	252	2	Q800I4_LEPOS	Q800i4 lepisosteus
11	778.5	61.4	252	2	Q800I5_AMICA	Q800i5 amia calva
12	682	53.8	250	1	STC_ANGAU	P18301 anguilla au
13	662.5	52.2	256	1	STC_ONCKI	Q08264 oncorhynchu
14	662.5	52.2	256	1	STC_ONCMY	P43648 oncorhynchu
15	660	52.1	249	2	Q4R1C1_CATCO	Q4r1c1 catostomus
16	654	51.6	249	2	Q98TB7_9TELE	Q98tb7 osteoglossu
17	653	51.5	249	2	Q6NYL8_BRARE	Q6nyl8 brachydanio
18	653	51.5	249	2	Q6PHV3_BRARE	Q6phv3 brachydanio
19	649	51.2	249	2	Q5IRA8_BRARE	Q5ira8 brachydanio
20	634	50.0	249	2	Q4R1C3_9TELE	Q4r1c3 gnathonemus
21	626.5	49.4	251	2	Q4R1C2_PANBU	Q4r1c2 pantodon bu
22	617	48.7	179	1	STC_ONCKE	P43647 oncorhynchu
23	603.5	47.6	251	2	Q5SBH7_PLAFE	Q5sbh7 platichthys
24	593	46.8	254	2	Q5IRB0_FUGRU	Q5irb0 fugu rubrip
25	583	46.0	255	2	Q4R1C0_9PERO	Q4r1c0 micropterus
26	572	45.1	204	2	Q4S1S9_TETNG	Q4s1s9 tetraodon n
27	425	33.5	119	2	Q4RCR1_TETNG	Q4rcr1 tetraodon n
28	371	29.3	294	2	Q4RN85_TETNG	Q4rn85 tetraodon n
29	361.5	28.5	283	2	Q5IRA9_FUGRU	Q5ira9 fugu rubrip
30	356	28.1	283	2	Q5IRA7_BRARE	Q5ira7 brachydanio
31	354.5	28.0	296	1	STC2_MOUSE	O88452 mus musculu
32	354.5	28.0	296	2	Q9DCS6_MOUSE	Q9dcs6 mus musculu
33	354.5	28.0	296	2	Q5SS12_MOUSE	Q5ss12 mus musculu
34	354	27.9	302	1	STC2_HUMAN	O76061 homo sapien
35	354	27.9	302	2	Q6FHC9_HUMAN	Q6fhc9 homo sapien
36	352	27.8	302	1	STC2_MACNE	O97561 macaca neme
37	349	27.5	296	1	STC2_RAT	Q9r0k8 rattus norv
38	340	26.8	302	1	STC2_PONPY	Q5rat2 pongo pygma
39	295.5	23.3	198	2	Q4RRX5_TETNG	Q4rrx5 tetraodon n
40	181.5	14.3	197	1	STC2_CAVPO	P57675 cavia porce
41	156	12.3	40	1	STC_ONCNE	P43649 oncorhynchu
42	104.5	8.2	1207	2	Q4UBC6_THEAN	Q4ubc6 theileria a
43	104	8.2	1044	2	Q7QT48_GIALA	Q7qt48 giardia lam
44	102	8.0	473	2	Q9SZ16_ARATH	Q9sz16 arabidopsis
45	99	7.8	1001	2	Q5CUF1_CRYPV	Q5cuf1 cryptospori

ALIGNMENTS

RESULT 1
STC1_HUMAN
ID STC1_HUMAN STANDARD; PRT; 247 AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Stanniocalcin-1 precursor (STC-1).
GN Name=STC1; Synonyms=STC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Fibrosarcoma, and Lung carcinoma;
RX MEDLINE=96077825; PubMed=7489828; DOI=10.1016/0303-7207(95)03601-3;
RA Chang A.C.-M., Janosi J., Hulsbeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone
RT stanniocalcin.";
RL Mol. Cell. Endocrinol. 112:241-247(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Fetal lung;
RX MEDLINE=96312491; PubMed=8700837; DOI=10.1073/pnas.93.5.1792;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral
RT metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon, Kidney, and Stomach;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROTEIN SEQUENCE OF 18-32.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC       therefore prevent hypercalcemia.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, with the highest
CC       levels in ovary, prostate, heart, kidney and thyroid. In the
CC       kidney, expression is confined to the nephron, specifically in the
CC       distal convoluted tubule and in the collecting tubule. Not
CC       detected in the brain, liver, spleen, peripheral blood leukocytes
CC       and adrenal medulla.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U25997; AAC09472.1; -; mRNA.
DR   EMBL; U46768; AAA88903.1; -; mRNA.
DR   EMBL; AF242179; AAL79522.1; -; Genomic_DNA.
DR   EMBL; BC029044; AAH29044.1; -; mRNA.
DR   Ensembl; ENSG00000159167; Homo sapiens.
DR   HGNC; HGNC:11373; STC1.
DR   H-InvDB; HIX0007390; -.
DR   MIM; 601185; -.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007584; P:response to nutrients; TAS.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Direct protein sequencing; Glycoprotein; Hormone; Signal.
FT   SIGNAL        1     17
FT   PROPEP       18     33       Potential.
FT   CHAIN        34    247       Stanniocalcin-1.
FT   CARBOHYD     62     62       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     45     59       By similarity.
FT   DISULFID     54     74       By similarity.
FT   DISULFID     65    114       By similarity.
FT   DISULFID     98    128       By similarity.
FT   DISULFID    135    170       By similarity.
FT   DISULFID    202    202       Interchain (By similarity).
SQ   SEQUENCE   247 AA;  27621 MW;  1E4A8BD861B49AED CRC64;

  Query Match           100.0%;  Score 1268;  DB 1;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-99;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 2
STC1_MOUSE
ID   STC1_MOUSE     STANDARD;      PRT;   247 AA.
AC   O55183;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Stanniocalcin-1 precursor (STC-1).
GN   Name=Stc1; Synonyms=Stc;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=BALB/c;
RX   MEDLINE=97179050; PubMed=9027337; DOI=10.1016/S0303-7207(96)03929-9;
RA   Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
RT   "Molecular cloning and characterization of mouse stanniocalcin cDNA.";
RL   Mol. Cell. Endocrinol. 124:185-187(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC       therefore prevent hypercalcemia (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U47815; AAC00050.1; -; Genomic_DNA.
DR   EMBL; BC021425; AAH21425.1; -; mRNA.
DR   Ensembl; ENSMUSG00000014813; Mus musculus.
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DR   MGI; MGI:109131; Stc1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0030320; P:monovalent inorganic anion homeostasis; TAS.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Glycoprotein; Hormone; Signal.
FT   SIGNAL        1     18       Potential.
FT   PROPEP       19     33       Potential.
FT   CHAIN        34    247       Stanniocalcin-1.
FT   CARBOHYD     62     62       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     45     59       By similarity.
FT   DISULFID     54     74       By similarity.
FT   DISULFID     65    114       By similarity.
FT   DISULFID     98    128       By similarity.
FT   DISULFID    135    170       By similarity.
FT   DISULFID    202    202       Interchain (By similarity).
SQ   SEQUENCE   247 AA;  27480 MW;  DAD30D08575A513B CRC64;

  Query Match             97.3%;  Score 1234;  DB 1;  Length 247;
  Best Local Similarity   96.4%;  Pred. No. 8.9e-97;
  Matches  238;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:|||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

Qy        241 RTSHESA 247
              ||| |||
Db        241 RTSQESA 247


RESULT 3
STC1_RAT
ID   STC1_RAT       STANDARD;      PRT;   247 AA.
AC   P97574;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Stanniocalcin-1 precursor (STC-1).
GN   Name=Stc1; Synonyms=Stc;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA   Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC       therefore prevent hypercalcemia (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U62667; AAB39541.1; -; mRNA.
DR   EMBL; BC078803; AAH78803.1; -; mRNA.
DR   Ensembl; ENSRNOG00000015075; Rattus norvegicus.
DR   RGD; 621776; Stc1.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0001503; P:ossification; IDA.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Glycoprotein; Hormone; Signal.
FT   SIGNAL        1     18       Potential.
FT   PROPEP       19     33       Potential.
FT   CHAIN        34    247       Stanniocalcin-1.
FT   CARBOHYD     62     62       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     45     59       By similarity.
FT   DISULFID     54     74       By similarity.
FT   DISULFID     65    114       By similarity.
FT   DISULFID     98    128       By similarity.
FT   DISULFID    135    170       By similarity.
FT   DISULFID    202    202       Interchain (By similarity).
SQ   SEQUENCE   247 AA;  27507 MW;  DAC2FD08575A513B CRC64;

  Query Match             97.1%;  Score 1231;  DB 1;  Length 247;
  Best Local Similarity   96.0%;  Pred. No. 1.6e-96;
  Matches  237;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:|||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

Qy        241 RTSHESA 247
              ||| |:|
Db        241 RTSQENA 247


RESULT 4
Q71UE3_MOUSE
ID   Q71UE3_MOUSE PRELIMINARY;      PRT;   247 AA.
AC   Q71UE3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stanniocalcin.
GN   Name=Stc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMattia G.E.;
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RT   "Comparative Analysis of Mammalian Stanniocalcin Genes.";
RL   Endocrinology 139:4717-4725(1998).
DR   EMBL; AF099098; AAC72394.1; -; mRNA.
DR   MGI; MGI:109131; Stc1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0030320; P:monovalent inorganic anion homeostasis; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SQ   SEQUENCE   247 AA;  27495 MW;  CA2DEDE659BAAFCB CRC64;

  Query Match             96.8%;  Score 1228;  DB 2;  Length 247;
  Best Local Similarity   96.0%;  Pred. No. 2.9e-96;
  Matches  237;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:|||||||||||||||||:| ||||||||||||||||||||||||||||||||
Db        121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQQPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

Qy        241 RTSHESA 247
              ||| |||
Db        241 RTSQESA 247


RESULT 5
STC1_BOVIN
ID   STC1_BOVIN     STANDARD;      PRT;   247 AA.
AC   Q9N0T1;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Stanniocalcin-1 precursor (STC-1).
GN   Name=STC1; Synonyms=STC;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Ovary;
RA   DiMattia G.E.;
RT   "Bovine stanniocalcin cDNA sequence.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC       therefore prevent hypercalcemia (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF257506; AAF68996.1; -; mRNA.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Glycoprotein; Hormone; Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    247       Stanniocalcin-1.
FT   CARBOHYD     24     24       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     62     62       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     45     59       By similarity.
FT   DISULFID     54     74       By similarity.
FT   DISULFID     65    114       By similarity.
FT   DISULFID     98    128       By similarity.
FT   DISULFID    135    170       By similarity.
FT   DISULFID    202    202       Interchain (By similarity).
SQ   SEQUENCE   247 AA;  27555 MW;  F9942A715E2A3DE0 CRC64;

  Query Match             94.6%;  Score 1199;  DB 1;  Length 247;
  Best Local Similarity   94.7%;  Pred. No. 8.5e-94;
  Matches  234;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:||||||||||||||||| ||||||||||||:||||||||||||||||||||
Db          1 MLQNSAVILVLVISASATHEAEQNDSVSLRKSRVAAQNSAEVIRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |||||||||:|||||:||||||||||||||||||||||||||||||||:||||||||||
Db        121 IAEVQEECYTKLNVCSVAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLDCDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||| |  |||||||| ||||||||||||||  ||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAHTQQRADFNRRRANEPQKLKVLLRNLRGEVASPSHIK 240

Qy        241 RTSHESA 247
              ||| |||
Db        241 RTSQESA 247


RESULT 6
Q7TSN9_MOUSE
ID   Q7TSN9_MOUSE PRELIMINARY;      PRT;   246 AA.
AC   Q7TSN9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Stanniocalcin 1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvJ;
RA   Chang A.C., Cha J., Reddel R.R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF512563; AAP47156.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
SQ   SEQUENCE   246 AA;  27423 MW;  4101C37EB6D743B2 CRC64;

  Query Match             94.0%;  Score 1192.5;  DB 2;  Length 246;
  Best Local Similarity   93.9%;  Pred. No. 3e-93;
  Matches  232;  Conservative    7;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| |||||||||||||||||||||||||||||| ::  | ||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSACRLAAG-FACL 59
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         60 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        120 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 179

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        180 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 239

Qy        241 RTSHESA 247
              ||| |||
Db        240 RTSQESA 246
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RESULT 7
Q5XGL3_XENLA
ID Q5XGL3_XENLA PRELIMINARY; PRT; 251 AA.
AC Q5XGL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC495194 protein.
GN Name=LOC495194;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC084424; AAH84424.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SQ SEQUENCE 251 AA; 27823 MW; C0C00D19FB700E19 CRC64;

```
  Query Match             68.8%;  Score 873;  DB 2;  Length 251;
  Best Local Similarity   70.7%;  Pred. No. 4.8e-66;
  Matches  164;  Conservative   38;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          5 SAVLL--VLVISASA-THEAEQNDS-VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              :|:||  ||:|| || ::: : ||| :  || |:|: :| ||||||| ||||||||||||
Db          5 TALLLLPVLLISVSAGSYDTDPNDSQLGGRKGRLASHSSVEVVRCLNGALQVGCGAFACL 64

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||:||||||||||||| ||||||||||||:||||||:|||||: |||
Db         65 ENSTCDTDGMYDICKAFLYSAAKFDTQGKVFVKESLKCIANGITSKVFLSIRRCSSLQRM 124

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:|||::||:||::|::|: || ||||||||| |||||||| |:|:||:|||:||| ::
Db        125 ISEVQQDCYTKLDICTVAQYNPNAITEVVQLPQHFSNRYYNTLLRNLLDCDEETVSAVKS 184

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGE 232
              ||||:||||:|:|| :|| | |:|  || ||||:|  |||||:: |||||||
Db        185 SLMEQIGPNLANLFQVLQGDKCSQIQPRMDFNRKRNIEPQKLRIYLRNLRGE 236
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RESULT 8
Q6DFI8_XENLA
ID Q6DFI8_XENLA PRELIMINARY; PRT; 253 AA.
AC Q6DFI8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Stc1-prov protein.
GN Name=stc1-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).

```
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076749; AAH76749.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SQ   SEQUENCE   253 AA;  28127 MW;  DFC93366DA31765D CRC64;

  Query Match             67.1%;  Score 851;  DB 2;  Length 253;
  Best Local Similarity   69.6%;  Pred. No. 3.6e-64;
  Matches  160;  Conservative   37;  Mismatches   31;  Indels    2;  Gaps    2;

Qy          8 LLVLVISASATHEAEQNDS-VSPRKS-RVAAQNSAEVVRCLNSALQVGCGAFACLENSTC 65
              ||:|    : ::::: ||| :  ||  |:|:| | ||||||| ||||||||||||||:|| 
Db         12 LLLLNSVCTGSYDSDPNDSQLGIRKGIRLASQISVEVVRCLNGALQVGCGAFACLENTTC 71

Qy         66 DTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQ 125
              ||||:|||||:|||||||||||||| ||||||||||||||||:|||||: ||||:||| 
Db         72 DTDGLYDICKAFLYSAAKFDTQGKVFVKESLKCIANGVTSKVFLSIRRCSSQQRMISEVQ 131

Qy        126 EECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEK 185
              ::||:|:::|::|: ||:|||||| || |||||||| |:||||:|||:||| :: ||||: 
Db        132 QDCYTKMDICTVAQYNPDAITEVVHLPQHFSNRYYNTLLRSLLDCDEETVSAVKSSLMEQ 191

Qy        186 IGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDS 235
              ||||:|||| :|| | |||  || ||||:|  :||||:| |||||||  | 
Db        192 IGPNLASLFQVLQGDKCAQIQPRMDFNRKRNIDPQKLRVYLRNLRGESSS 241


RESULT 9
Q71UE5_HUMAN
ID   Q71UE5_HUMAN PRELIMINARY;      PRT;   157 AA.
AC   Q71UE5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stanniocalcin (Fragment).
GN   Name=STC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99008615; PubMed=9794484; DOI=10.1210/en.139.11.4714;
RA   Varghese R., Wong C.K., Deol H., Wagner G.F., DiMattia G.E.;
RT   "Comparative analysis of mammalian stanniocalcin genes.";
RL   Endocrinology 139:4714-4725(1998).
DR   EMBL; AF098463; AAC97949.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  17094 MW;  E22F2A6067966C3E CRC64;

  Query Match             62.9%;  Score 797;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-60;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSN 157
              |||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSN 157


RESULT 10
Q800I4_LEPOS
ID   Q800I4_LEPOS PRELIMINARY;      PRT;   252 AA.
AC   Q800I4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Stanniocalcin precursor.
GN   Name=STC;
OS   Lepisosteus osseus (Long-nosed gar).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC   Lepisosteus.
OX   NCBI_TaxID=34771;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14697312; DOI=10.1016/j.ygcen.2003.09.019;
RA   Amemiya Y., Youson J.H.;
RT   "Primary structure of stanniocalcin in two basal Actinopterygii.";
RL   Gen. Comp. Endocrinol. 135:250-257(2004).
DR   EMBL; AB106623; BAC66164.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW   Signal.
FT   SIGNAL        1     32       Potential.
FT   CHAIN        33    252       Potential.
SQ   SEQUENCE   252 AA;  27936 MW;  2C99E88DCCED2E33 CRC64;

  Query Match             61.5%;  Score 779.5;  DB 2;  Length 252;
  Best Local Similarity   59.8%;  Pred. No. 4.4e-58;
  Matches  152;  Conservative   44;  Mismatches   49;  Indels    9;  Gaps    3;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||: : :||:||:  || :| :||:| |||::||:  : ::| ||||||||||||||||| 
Db          1 MLRKTGILLLLVLLTSA-YELDQNESFSPRRTRVSTHSPSDVARCLNSALQVGCGAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||:|||||||||||||||| ||||||||||:|||||  |||||||||| 
Db         60 ENSTCDTDGMHDICKSFLYSAAKFDTQGKVFVKESLKCIANGITSKVFLTIRRCSTFQRM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:||||||||||::| :|| ||:||:|| |||:|| ||||::|::||:|||::||| :| 
Db        120 ISEVQEECYSKLDICGVAKLNPDAISEVAQLPSHFPNRYYSKLLQSLMECDDETVSLVRS 179

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRAD-------FNRRRTNEPQKLKVLLRNLRGEE 233
              ||: ::|| || || :||:  |  :   :          | |    |   | :  ||| | 
Db        180 SLVSRLGPEMAMLFQLLQSKPCPSSSSLSSPAGAEGRGNWRWPIGPHVFK-MQPNLRREP 238

Qy        234 DSPSHIKRTSHESA 247
               :    ||:: :|: 
Db        239 STLFSKKRSADDSS 252


RESULT 11
Q800I5_AMICA
ID   Q800I5_AMICA PRELIMINARY;      PRT;   252 AA.
AC   Q800I5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE   Stanniocalcin precursor.
GN   Name=STC;
OS   Amia calva (Bowfin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX   NCBI_TaxID=7924;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14697312; DOI=10.1016/j.ygcen.2003.09.019;
RA   Amemiya Y., Youson J.H.;
RT   "Primary structure of stanniocalcin in two basal Actinopterygii.";
RL   Gen. Comp. Endocrinol. 135:250-257(2004).
DR   EMBL; AB106622; BAC66163.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW   Signal.
FT   SIGNAL        1     32       Potential.
FT   CHAIN        33    252       Potential.
SQ   SEQUENCE   252 AA;  27868 MW;  B9D9663610DF0B5D CRC64;

  Query Match             61.4%;  Score 778.5;  DB 2;  Length 252;
  Best Local Similarity   69.8%;  Pred. No. 5.3e-58;
  Matches  141;  Conservative   37;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||  : :||:||:  || :| :||:| |||::||:| :|::| ||||||||||||||||
Db          1 MLHKTGILLLLVLLTSA-YELDQNESFSPRRTRVSAHSSSDVARCLNSALQVGCGAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||:||||||||||||||||| ||||||||||||:|||||| ||||||||||
Db         60 ENSTCDTDGMHDICKSFLYSAAKFDTQGKVFVKESLKCIANGITSKVFLTIRRCSTFQRM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:|||||||:||::| :|: |||||:|| |||:|| ||||::|::||:||||:||| :|
Db        120 ISEVQEECYTKLDICEVARLNPEAISEVAQLPSHFPNRYYSKLLQSLMECDEETVSVVRS 179

Qy        181 SLMEKIGPNMASLFHILQTDHC 202
              :|: ::|| |: || :||:  |
Db        180 NLVSRLGPEMSMLFQLLQSKPC 201


RESULT 12
STC_ANGAU
ID   STC_ANGAU      STANDARD;      PRT;   250 AA.
AC   P18301;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   Name=STC;
OS   Anguilla australis (Australian eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC   Anguilla.
OX   NCBI_TaxID=7940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 33-57.
RX   MEDLINE=88083961; PubMed=3319739; DOI=10.1016/0303-7207(87)90149-3;
RA   Butkus A., Roche P.J., Fernley R.T., Haralambidis J., Penschow J.D.,
RA   Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;
RT   "Purification and cloning of a corpuscles of Stannius protein from
RT   Anguilla australis.";
RL   Mol. Cell. Endocrinol. 54:123-133(1987).
RN   [2]
RP   SEQUENCE REVISION.
RA   Roche P.J.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC       Upon release into the circulation, it lowers calcium transport by
CC       the gills, thereby reducing its rate of influx from the
CC       environment into the extracellular compartment. STC also
CC       stimulates phosphate reabsorption by renal proximal tubules. The
CC       consequence of this action is increased levels of plasma
CC       phosphate, which combines with excess calcium and promotes its
CC       disposal into bone and scales.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- TISSUE SPECIFICITY: Corpuscles of Stannius.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M36967; AAB91483.1; -; mRNA.
DR   PIR; A54648; A54648.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Direct protein sequencing; Glycoprotein; Hormone; Signal.
FT   SIGNAL        1     17       Potential.
FT   PROPEP       18     32       Potential.
FT   CHAIN        33    250       Stanniocalcin.
FT   CARBOHYD     61     61       N-linked (GlcNAc. . .) (Probable).
FT   DISULFID     44     58       By similarity.
FT   DISULFID     53     73       By similarity.
FT   DISULFID     64    113       By similarity.
FT   DISULFID     97    127       By similarity.
FT   DISULFID    134    169       By similarity.
FT   DISULFID    201    201       Interchain (By similarity).
SQ   SEQUENCE   250 AA;  27174 MW;  BB972BD951F75B3E CRC64;

  Query Match             53.8%;  Score 682;  DB 1;  Length 250;
  Best Local Similarity   54.3%;  Pred. No. 8.6e-50;
  Matches  138;  Conservative   47;  Mismatches   57;  Indels   12;  Gaps    6;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||: | ::| ||:  :| :| :::: :||| :| :| : ::| |||| |||||| |||||
Db          1 MLRMSGLILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              :||||:||||::||:|||: |||||||| ||||||||||:|||||| |||||:||:|
Db         60 DNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:||||||||||::||:|: ||||: || |:|: | ||||: |::||| ||||||  :|
Db        120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179

Qy        181 SLMEKIGPNMASLFHILQTDHC-----AQTHP-RADFNRRRTNEPQKLKVLLRNLRGEED 234
              |: :: | |  || :|||  |        | |  |  : |     |   |:  |||  :
Db        180 GLVSRLEPEMGVLFQLLQTKACPPSAAGGTGPVGAGGSWRWPMGPPMFKI-QPNLRSRD- 237

Qy        235 SPSHI--KRTSHES 246
              |:|:  |: |  |
Db        238 -PTHLFAKKRSTSS 250


RESULT 13
STC_ONCKI
ID   STC_ONCKI      STANDARD;      PRT;   256 AA.
AC   Q08264;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   Name=STC;
OS   Oncorhynchus kisutch (Coho salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8019;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93246046; PubMed=1363790; DOI=10.1016/0303-7207(92)90095-N;
RA   Wagner G.F., Dimattia G.E., Davie J.R., Copp D.H., Friesen H.G.;
RT   "Molecular cloning and cDNA sequence analysis of coho salmon
RT   stanniocalcin.";
RL   Mol. Cell. Endocrinol. 90:7-15(1992).
RN   [2]
RP   PROTEIN SEQUENCE OF 34-73.
RX   MEDLINE=89065334; PubMed=3197944;
RA   Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
RA   Friesen H.G.;
RT   "Comparative biochemistry and physiology of teleocalcin from sockeye
RT   and coho salmon.";
RL   Gen. Comp. Endocrinol. 72:237-246(1988).
CC   -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC       Upon release into the circulation, it lowers calcium transport by
CC       the gills, thereby reducing its rate of influx from the
CC       environment into the extracellular compartment. STC also
CC       stimulates phosphate reabsorption by renal proximal tubules. The
CC       consequence of this action is increased levels of plasma
CC       phosphate, which combines with excess calcium and promotes its
CC       disposal into bone and scales.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
CC       Stannius.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; S59519; AAB26419.1; -; mRNA.
DR   PIR; B60841; B60841.
DR   PIR; I51197; I51197.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Calcium; Calcium transport; Direct protein sequencing; Glycoprotein;
KW   Hormone; Ion transport; Signal; Transport.
FT   SIGNAL       1     18       Potential.
FT   PROPEP      19     33       By similarity.
FT   CHAIN       34    256       Stanniocalcin.
FT   CARBOHYD    62     62       N-linked (GlcNAc. . .).
SQ   SEQUENCE   256 AA;  28074 MW;  E688B930B394A8D3 CRC64;

  Query Match             52.2%;  Score 662.5;  DB 1;  Length 256;
  Best Local Similarity   53.4%;  Pred. No. 4e-48;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||   ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: |||||  ||||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
               :|| :||  || |   :  :      |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241
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RESULT 14

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STC_ONCMY
ID   STC_ONCMY      STANDARD;      PRT;   256 AA.
AC   P43648; Q98SE1;
DT   01-NOV-1995 (Rel. 32, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   Name=STC;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RA   McCudden C.R., Wagner G.F.;
RT   "Rainbow trout ovarian stanniocalcin.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   PROTEIN SEQUENCE OF 34-66.
RC   TISSUE=Stannius corpuscules;
RX   MEDLINE=88196801; PubMed=3360288;
RA   Lafeber F.P.J.G., Hanssen R.G.J.M., Choy Y.M., Flik G.,
RA   Herrmann-Erlee M.P.M., Pang P.K.T., Wendelaar Bonga S.E.;
RT   "Identification of hypocalcin (teleocalcin) isolated from trout
RT   Stannius corpuscles.";
RL   Gen. Comp. Endocrinol. 69:19-30(1988).
CC   -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC       Upon release into the circulation, it lowers calcium transport by
CC       the gills, thereby reducing its rate of influx from the
CC       environment into the extracellular compartment. STC also
CC       stimulates phosphate reabsorption by renal proximal tubules. The
CC       consequence of this action is increased levels of plasma
CC       phosphate, which combines with excess calcium and promotes its
CC       disposal into bone and scales.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
CC       Stannius.
CC   -!- SIMILARITY: Belongs to the stanniocalcin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF326317; AAK01423.1; -; mRNA.
DR   EMBL; AF326318; AAK01424.1; -; mRNA.
DR   InterPro; IPR004978; Stanniocalcin.
DR   PANTHER; PTHR11245; Stanniocalcin; 1.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Calcium; Calcium transport; Direct protein sequencing; Glycoprotein;
KW   Hormone; Ion transport; Signal; Transport.
FT   SIGNAL       1     18       Potential.
FT   PROPEP      19     33
FT   CHAIN       34    256       Stanniocalcin.
FT   CARBOHYD    62     62       N-linked (GlcNAc. . .).
FT   VARIANT     41     41       D -> E.
SQ   SEQUENCE   256 AA;  28104 MW;  E688A0E0B394A8D3 CRC64;

  Query Match             52.2%;  Score 662.5;  DB 1;  Length 256;
  Best Local Similarity   53.4%;  Pred. No. 4e-48;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||   ||||  |||||:||||||||
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Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
               :|| :||  || |   :   :     |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


RESULT 15
Q4R1C1_CATCO
ID   Q4R1C1_CATCO PRELIMINARY;      PRT;   249 AA.
AC   Q4R1C1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Stanniocalcin precursor.
GN   Name=STC;
OS   Catostomus commersoni (White sucker).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Catostomidae; Catostomus.
OX   NCBI_TaxID=7971;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Corpuscle of Stannius;
RA   Amemiya Y., Marra L.E., Youson J.H.;
RT   "primary structure of White sucker stanniocalcin.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB218776; BAD99602.1; -; mRNA.
KW   Signal.
FT   SIGNAL        1     31       Potential.
FT   CHAIN        32    249       Potential.
SQ   SEQUENCE   249 AA;  27673 MW;  6E1034172216D028 CRC64;

  Query Match             52.1%;  Score 660;  DB 2;  Length 249;
  Best Local Similarity   59.9%;  Pred. No. 6.4e-48;
  Matches  121;  Conservative   34;  Mismatches   45;  Indels    2;  Gaps    2;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||  |  ||: |:  || :|  | |    ||::| :| :  :| |||| ||||||  ||||
Db          1 MLLKSGFLLLFVLVTSA-YETNQ-DPAQPRRARFSANSPTDVARCLNGALQVGCATFACL 58

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||::|| :| ::|| |:| || |||||:||||||:|||||  ||||||||:|
Db         59 ENSTCDTDGMHEICNAFFHTAAIFNTDGKTFVKESIKCIANGITSKVFQTIRRCSTFQKM 118

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||| ||::| :|: ||||| :|||:|||| |||| |: ||:|||:| |  :|
Db        119 IAEVQEECYKKLDICEVARSNPEAIGDVVQVPNHFPNRYYSTLLESLMECDDDIVEVVRA 178

Qy        181 SLMEKIGPNMASLFHILQTDHC 202
               |: ::||:| :|| :||   |
Db        179 GLVSRLGPDMVTLFQLLQNKPC 200


Search completed: April  4, 2006, 14:14:37
Job time : 233 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:10:59 ; Search time 40 Seconds
(without alignments)
594.139 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680.5	53.7	263	2	A54648	stanniocalcin prec
2	662.5	52.2	256	2	I51197	stanniocalcin - co
3	354	27.9	302	2	JE0357	stanniocalcin homo
4	150	11.8	40	2	B60841	teleocalcin - coho
5	149	11.8	40	2	A60841	teleocalcin - sock
6	123	9.7	33	2	S06337	teleocalcin - rain
7	102	8.0	473	2	T04799	hypothetical prote
8	94	7.4	1105	2	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2	T50776	hypothetical prote
10	90.5	7.1	783	2	T38690	probable regulator
11	89.5	7.1	1126	2	T01491	ubiquitin-protein
12	89	7.0	305	2	T08121	peroxidase (EC 1.1
13	88	6.9	473	2	T45954	hypothetical prote
14	87.5	6.9	1465	2	S45628	DNA-directed DNA p
15	86	6.8	470	2	F86526	Mg++ transporter [
16	86	6.8	470	2	H72097	mg++ transporter (
17	86	6.8	510	2	T45952	hypothetical prote
18	86	6.8	556	2	S51858	probable membrane
19	86	6.8	581	2	S58201	probable membrane
20	83	6.5	250	2	D69215	conserved hypothet
21	83	6.5	250	2	S30584	hypothetical prote
22	83	6.5	365	2	T06693	hypothetical prote
23	83	6.5	1093	2	T50652	AP-3 complex beta3
24	83	6.5	1094	2	T50651	AP3-complex beta-3
25	82.5	6.5	869	2	A88710	protein C43G2.2 [i
26	82.5	6.5	1483	2	S30015	hypothetical prote
27	82.5	6.5	1757	2	T05204	hypothetical prote
28	82.5	6.5	2335	2	T40186	probable phosphati
29	82.5	6.5	2535	2	T04824	hypothetical prote
30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	P64640	conserved hypothet
34	81.5	6.4	708	1	TFBOL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	JC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1
A54648
stanniocalcin precursor - Australian eel
N;Alternate names: Stannius corpuscle secretory protein
C;Species: Anguilla australis (Australian eel)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A54648
R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.;
Mol. Cell. Endocrinol. 54, 123-133, 1987
A;Title: Purification and cloning of a corpuscles of Stannius protein from Anguilla aus
A;Reference number: A54648; MUID:88083961; PMID:3319739
A;Accession: A54648
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-263 <BUT>
A;Cross-references: UNIPROT:P18301; UNIPARC:UPI000002BEB5
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-263/Product: stanniocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;
Best Local Similarity 61.4%; Pred. No. 2.3e-51;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||: | ::| ||:  :| :| :::: :||| :| :| : ::| |||| |||||| |||||
Db          1 MLRMSGLILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              :||||:||||::||:|||: ||||||||| ||||||||||||:|||||| |||||:||:|
Db         60 DNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:||||||||||::||:|: |||||: || |:|: | |||||: |::||| |||||  :|
Db        120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179

Qy        181 SLMEKIGPNMASLFHILQTDHC 202
              |: :: | |  || :|||  |
Db        180 GLVSRLEPEMGVLFQLLQTKAC 201
```

RESULT 2
I51197
stanniocalcin - coho salmon
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51197
R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.
Mol. Cell. Endocrinol. 90, 7-15, 1992
A;Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.
A;Reference number: I51197; MUID:93246046; PMID:1363790
A;Accession: I51197
A;Status: preliminary; translated from GB/EMBL/DDBJ

```
A;Molecule type: mRNA
A;Residues: 1-256 <WAG>
A;Cross-references: UNIPROT:Q08264; UNIPARC:UPI00001360D2; GB:S59519; NID:g299926; PIDN:

  Query Match            52.2%;  Score 662.5;  DB 2;  Length 256;
  Best Local Similarity  53.4%;  Pred. No. 8e-50;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
               :|| :||  || |   :  :     |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


RESULT 3
JE0357
stanniocalcin homolog - human
N;Alternate names: STC2
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0357
R;Ishibashi, K.; Miyamoto, K.; Taketani, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M
Biochem. Biophys. Res. Commun. 250, 252-258, 1998
A;Title: Molecular cloning of a second human stanniocalcin homologue (STC2).
A;Reference number: JE0357; MUID:98440784; PMID:9753616
A;Accession: JE0357
A;Molecule type: mRNA
A;Residues: 1-302 <ISH>
A;Cross-references: UNIPROT:O76061; UNIPARC:UPI00001360B8; DDBJ:AB012664; NID:g3702223;
C;Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
C;Genetics:
A;Introns: 51/1 98/3 169/2

  Query Match            27.9%;  Score 354;  DB 2;  Length 302;
  Best Local Similarity  32.4%;  Pred. No. 4.6e-23;
  Matches   83;  Conservative   45;  Mismatches  102;  Indels   26;  Gaps    4;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::         ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::| ||| | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----------------- 222
              |:  :   |  ||  ||       | | |   |:   :  ||
Db        192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy        223 KVLLRNLRGEEDSPSH 238
              :   |  :||  | ||
Db        252 RETGRGAKGERGSKSH 267


RESULT 4
B60841
teleocalcin - coho salmon (fragment)
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sa
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: B60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
A;Cross-references: UNIPROT:Q08264; UNIPARC:UPI0000179B05
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim u
C;Keywords: disulfide bond; glycoprotein; hormone

  Query Match            11.8%;  Score 150;  DB 2;  Length 40;
  Best Local Similarity  66.7%;  Pred. No. 1.8e-06;
  Matches   26;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73
              :: : ::| |||| || |||| ||||| |||||||||:||
Db          2 SSNSPSDVARCLNGALAVGCGTFACLEXSTCDTDGMHDI 40


RESULT 5
A60841
teleocalcin - sockeye salmon (fragment)
C;Species: Oncorhynchus nerka (sockeye salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sa
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: A60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
A;Cross-references: UNIPROT:P43649; UNIPARC:UPI0000179B06
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim u
C;Keywords: disulfide bond; glycoprotein; hormone

  Query Match            11.8%;  Score 149;  DB 2;  Length 40;
  Best Local Similarity  76.5%;  Pred. No. 2.2e-06;
  Matches   26;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 AEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73
              ::| |||| || |||| ||||| |||||||:||
Db          7 SDVARCLNGALDVGCGTFACLEXSTCDTDGMHDI 40


RESULT 6
S06337
teleocalcin - rainbow trout (fragment)
N;Alternate names: hypocalcin
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
C;Accession: S06337
R;Lafeber, F.P.J.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Flik, G.; Herrmann-Erlee, M.P.M.; Pa
Gen. Comp. Endocrinol. 69, 19-30, 1988
A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius corpus
A;Reference number: S06337; MUID:88196801; PMID:3360288
A;Accession: S06337
A;Molecule type: protein
A;Residues: 1-33 <LAF>
A;Cross-references: UNIPARC:UPI0000179B07
A;Note: 7-Glu was also found
C;Keywords: dimer; glycoprotein; hormone
F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             9.7%;  Score 123;  DB 2;  Length 33;
  Best Local Similarity  65.6%;  Pred. No. 0.00031;
  Matches   21;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCD 66
              :: : ::| |||| || |||| ||||||||||
```

```
Db          2 SSNSPSDVARCLNGALAVGCGTFACLENSTCD 33


RESULT 7
T04799
hypothetical protein F10M23.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04799
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15385
A;Accession: T04799
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: UNIPROT:Q9SZ16; UNIPARC:UPI00000A64C3; EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
C;Genetics:
A;Map position: 4
A;Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3
A;Note: F10M23.100

  Query Match             8.0%;  Score 102;  DB 2;  Length 473;
  Best Local Similarity   21.0%;  Pred. No. 0.48;
  Matches   50;  Conservative   43;  Mismatches   67;  Indels   78;  Gaps   11;

Qy         26 SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT----DGMYDICKSF-LYS 80
              :|  :|  :||:: ||::: |:          | :| |   |        ||| |  |:
Db         50 NVYKKKVELAAKSRAELLQTLSD---------ATVELSNLTTALGEKSYIDICDSMSLFP 100

Qy         81 AAKFDTQGKAFVKESLKCIA----------------------------------NG-- 102
                | |   :|| |  ||                                    ||
Db        101 LQPDKTSGT--IKEQLSAIAPALEQLWQQKEERVRAFSDVQSQIQKICEEIAGGLNNGPH 158

Qy        103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----------NVCSIAKRN-PEAITEV-- 148
              |  :  |:::|   ||| : |:|:|   :|          ::|:: : :    :|||
Db        159 VVDETDLSLKRLDDFQRKLQELQKEKSDRLQKVLEFVSTVHDLCAVLRLDFLSTVTEVHP 218

Qy        149 -------VQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
                    ||  :  ||    || :::|   || :  ::   ::::   :  |:::: |
Db        219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQRLKK--LQELATQLTDLWNLMDT 273


RESULT 8
T18295
Ap-3 adaptor complex beta3A chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18295
R;Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusi
Hum. Mol. Genet. 8, 323-330, 1999
A;Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the m
A;Reference number: Z18864; MUID:99135912; PMID:9931340
A;Accession: T18295
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1105 <FEN>
A;Cross-references: UNIPROT:Q9Z1T1; UNIPARC:UPI000002973F; EMBL:AF103809; NID:g3885987;
A;Experimental source: strain C3H/HeJ
C;Genetics:
A;Gene: Ap3b1
A;Map position: 13

  Query Match             7.4%;  Score 94;  DB 2;  Length 1105;
  Best Local Similarity   21.2%;  Pred. No. 6.5;
  Matches   55;  Conservative   40;  Mismatches  104;  Indels   60;  Gaps   11;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              :||:    :|: ::    |       :||:    |  |  :|| | |  :|      :
Db        308 LLQSRNAAVVMAVAQLYWH-------ISPKSE--AGVISKSLVRLLRSNREVQYIVLQNI 358

Qy         61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL---------- 109
                : :  ||::   ||| |  :   |  |    | |  :||       |

Db        359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy        110 ----------AIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE---VVQLPNHFS 156
                       | ||:|    |:|  | |:: | || :: |:   : |   |::
Db        418 DKQFAAATIQTIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 473

Qy        157 NRYYNRLVRSLLE-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
                :  ::| : :  |  ||   | |::  || |           | :    |
Db        474 PAQHGEIIRHMAKFLDSITVPVARASILWLIGEN-----------CERVPKIA------ 515

Qy        216 TNEPQKLKVLLRNLRGEED 234
                |  |: : ::   |:|
Db        516 ---PDVLRKMAKSFTSEDD 531


RESULT 9
T50776
hypothetical protein [imported] - Vitis vinifera
C;Species: Vitis vinifera
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50776
R;Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A;Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP protein
A;Reference number: Z25233
A;Accession: T50776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <MAT>
A;Cross-references: UNIPROT:P93798; UNIPARC:UPI0000135B10; EMBL:AB001375; PIDN:BAA19246
A;Experimental source: strain Shiraz

  Query Match             7.1%;  Score 90.5;  DB 2;  Length 289;
  Best Local Similarity   19.9%;  Pred. No. 2.6;
  Matches   41;  Conservative   33;  Mismatches   95;  Indels   37;  Gaps    5;

Qy          8 LLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT 67
              |  :: |: : ||| |  : :          :: | : ||  |        |:  |:|   :
Db         59 LSTVIQSSDSKHEAAQ--AYADAGHCYKKTSAKEAISCLEQA------AYLFLDNGRFNM 110

Qy         68 DG--------MYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQR 119
              |         :|:: ::|  :   |:     :  |      ||   :||     :   :|:
Db        111 AGKYYKEIAELYELEQNFEQAIIYFEKAADIYQSEEATTAANQCNAKVAQFAAQLEQYQK 170

Qy        120 MIAEVQEECYSKLN----------------VCSIAKRNPEAITEVVQL-----PNHFSNR 158
              |   ::    ||                :| : | :  |||  :        |      |
Db        171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPTFSGTR 230

Qy        159 YYNRLVRSLLECDEDTVSTIRDSLME 184
              |  ||       ||: |    |:: |
Db        231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256


RESULT 10
T38690
probable regulatory protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T38690
R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21805
A;Accession: T38690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-783 <BRO>
A;Cross-references: UNIPROT:O14130; UNIPARC:UPI000006AB27; EMBL:Z99568; PIDN:CAB16735.1
A;Experimental source: strain 972h-; cosmid c3C7
C;Genetics:
A;Gene: SPDB:SPAC3C7.04
A;Map position: 1
F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>
```

```
  Query Match             7.1%;  Score 90.5;  DB 2;  Length 783;
  Best Local Similarity   23.3%;  Pred. No. 8.6;
  Matches   56;  Conservative   34;  Mismatches   87;  Indels   63;  Gaps   12;

Qy         10 VLVISASATHEAEQNDSVSPRKSRV------AAQNSAEVVRCLNSALQVGCGAF------ 57
              ::::|         :|   |||  |:      ||::   :|  | :  |: | :|
Db        535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594

Qy         58 ---------ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI--------- 99
                       |:   |: |   ||  : |||  :  :|    |   : |
Db        595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy        100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCSIAKRNPEAITEVV 149
                  || ||:  |:|      :|| ||||      |:  |  |      ||  ::|
Db        651 ARSDGNGNTSQSGFMA------WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy        150 QLPNHFSNRYYNR------LVRSLLECDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
               |    |  ::        |  | |: | :  ::  | :  |  |::|   || :   ||
Db        705 NLGADVS--FFPTDDTSFLLDHSKLDDDLEKFASTLDPI--KTTPDLANDSSLLNWANTD 760


RESULT 11
T01491
ubiquitin-protein ligase homolog F17O7.15 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01491
R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li,
rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC F17O7 sequence.
A;Reference number: Z14334
A;Accession: T01491
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1126 <VYS>
A;Cross-references: UNIPROT:O64605; UNIPARC:UPI00000A614B; EMBL:AC003671; NID:g2833627;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: ATSP:F17O7.15
A;Map position: 1
A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

  Query Match             7.1%;  Score 89.5;  DB 2;  Length 1126;
  Best Local Similarity   22.1%;  Pred. No. 16;
  Matches   46;  Conservative   39;  Mismatches   76;  Indels   47;  Gaps    8;

Qy         14 SASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCD------- 66
              |:    :||   ||: ||       | ||:    |  ||:         ::  |:
Db        412 SSETQKDAESELSVARRK------NCAEL---YNIFLQLP-------QSDLCNLCMLLGY 455

Qy         67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
                 :| :|  :     |   | |   : |  :  :|:|::|      :   || |:|
Db        456 EGLSDKIYSLAGEVLKKLAAVDVTHRKFFTKELSELASGLSSSTVRVLATLSTTQKM--- 512

Qy        124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIR---- 179
                    | ||:|      :|  |:|: :  ::   :  | :  | |::  : ::
Db        513 -------SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 562

Qy        180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
                : | :::|  ::     || || | |
Db        563 ALEPLWQELGQCIS--MTELQLDHTAAT 588


RESULT 12
T08121
peroxidase (EC 1.11.1.7) - flax (fragment)
C;Species: Linum usitatissimum (flax)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08121
R;Omann, F.; Tyson, H.
submitted to the EMBL Data Library, February 1998
A;Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.
A;Reference number: Z16366
A;Accession: T08121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-305 <OMA>
A;Cross-references: UNIPROT:O65029; UNIPARC:UPI00000AA5D8; EMBL:AF049881; NID:g2944416;
A;Experimental source: cv. Stormont Cirrus
C;Genetics:
A;Gene: PER4
C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;23-103/Disulfide bonds: #status predicted
F;50/Active site: Arg #status predicted
F;54,181/Binding site: heme iron (His) (axial ligands) #status predicted
F;56-61/Disulfide bonds: #status predicted
F;109-301/Disulfide bonds: #status predicted
F;188-213/Disulfide bonds: #status predicted

  Query Match             7.0%;  Score 89;  DB 2;  Length 305;
  Best Local Similarity   21.9%;  Pred. No. 3.8;
  Matches   57;  Conservative   39;  Mismatches   92;  Indels   72;  Gaps   15;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGA-FACLE-NSTCDTD 68
              |::  :||   |:|    | :: |       :::  : : ::  | |  :| :  :    |
Db         65 LLLDDTATFTGEKN--AGPNQNSV---RGFDIIDTIKTRVEAACNATVSCADILALAARD 119

Qy         69 GMYDI-------------CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
              |: :              ::  |||              ||  | |  |:|   |
Db        120 GVVLVGGPTWTVPLGRRDARTASQSAANAQIPAPG---SSLGTITNLFTNKGLTARDVTI 176

Qy        111 --------IRRCSTFQRMIAEVQEECYSKLNV----CSIAKRN-PEA-----ITEVVQLP 152
                      ||:||:: |       |:  |:      :  : | |:|     :  :    |
Db        177 LSGAHTIGQARCTTFRQRI-------YNDTNIDPAFATTRRGNCPQAGAGANLAPLDGTP 229

Qy        153 NHFSNRYYNRLV--RSLLECDEDTVST-IRDSLMEKIGPNMASLFHILQTDHCAQ----- 204
                | ||||  ||  | ||  |::  :   :|:|:     | |:      ||  |
Db        230 TQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT----FATDFAAAMVRMG 285

Qy        205 -------THPRADFNRRRTN 217
                     |:    || || |
Db        286 NISPLTGTNGEIRFNCRRPN 305


RESULT 13
T45954
hypothetical protein F7J8.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45954
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Le
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23018
A;Accession: T45954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: UNIPROT:Q9LFC2; UNIPARC:UPI00000A92D2; EMBL:AL137189
A;Experimental source: cultivar Columbia; BAC clone F7J8
C;Genetics:
A;Map position: 5
A;Introns: 29/1; 428/3
A;Note: F7J8.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

  Query Match             6.9%;  Score 88;  DB 2;  Length 473;
  Best Local Similarity   22.6%;  Pred. No. 7.8;
  Matches   54;  Conservative   42;  Mismatches  103;  Indels   40;  Gaps   13;

Qy         27 VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLEN---STCD---TDGMYDICKS-FLY 79
              :   |::|    :  :|| |    :        || |   |  |    |  | ||   ||
Db         16 IDEEKNKVVLAEAGTIVRLLAKHRKSDPVTIGCLRNLYTSVVDMELDDFETDACKQMLLY 75
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Qy          80 SAAKFDTQGKAF-----VKESLKCIANGVTSKVFLAIRRCSTFQRMIAE----VQEEC-- 128
               : | : |       |||||       : |   | || |   : :    : ||
Db          76 PKNIREAQYRNFKLNIDTNESLKCFG----CRFFSICRMCSNFNTSLCKCGKLMNEEISF 131

Qy         129 --YSKLNVCSIAKRNPEA--ITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
                 | : :|  :  |: :  ||: ::| :  :    : |:::| :     || :|: :::
Db         132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST----SSLLQTLKDLGCADVSKLREQVLD 187

Qy         185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLLRNLRGEEDSPSHI 239
                ||     |  ::    |  |   |  |     : :|  :|:   | : :|:|  |  :
Db         188 -IG-----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV 240


RESULT 14
S45628
DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse
N;Alternate names: DNA polymerase alpha/DNA primase complex 180K chain
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S45628; A46642
R;Stadlbauer, F.; Brueckner, A.; Rehfuess, C.; Eckerskorn, C.; Lottspeich, F.; Foerster,
Eur. J. Biochem. 222, 781-793, 1994
A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
A;Reference number: S45628; MUID:94298818; PMID:8026492
A;Accession: S45628
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1465 <STA>
A;Cross-references: UNIPROT:P33609; UNIPARC:UPI0000020FBD; EMBL:D17384; NID:g397829; PID
R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.
J. Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase al
A;Reference number: A46642; MUID:93216788; PMID:8463324
A;Accession: A46642
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 4-1465 <MIY>
A;Cross-references: UNIPARC:UPI0000175787
A;Experimental source: FM3A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIP:129147)
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; nucleotidyltransferase; nucleus

  Query Match             6.9%;  Score 87.5;  DB 2;  Length 1465;
  Best Local Similarity   20.7%;  Pred. No. 33;
  Matches   34;  Conservative   32;  Mismatches   55;  Indels   43;  Gaps    7;

Qy           6 AVLLVLVISASAT-------HEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFA 58
               |||: | :   :|       |: |:||::    :::  :   :             |  |
Db        1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----------DCEKFK 1284

Qy          59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT------SKVFLAIR 112
               ||  | | |: :||     ::  :  | :   :   :: |  : :|      :|: : ||
Db        1285 CLCPS-CGTENIYD----NVFEGSGLDMEPSLYRCSNVDCKVSPLTFMVQLSNKLIMDIR 1339

Qy         113 RCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFS 156
               ||           :: |    :|      |   : : :|| |||
Db        1340 RCI----------KKYYDGWLIC----EEPTCCSRLRRLPLHFS 1369


RESULT 15
F86526
Mg++ transporter [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86526
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: UNIPROT:Q9Z8Q2; UNIPARC:UPI00000D40EA; GB:BA000008; NID:g8978660; PI
A;Experimental source: strain J138
C;Genetics:
A;Gene: mgtE
C;Superfamily: magnesium transport protein mgtE

  Query Match             6.8%;  Score 86;  DB 2;  Length 470;
  Best Local Similarity   22.9%;  Pred. No. 12;
  Matches   47;  Conservative   33;  Mismatches   61;  Indels   64;  Gaps   13;

Qy          56 AFACLENSTCDTD-GMYDICK--------SFLYSAAKFDTQGKAFVKESLKCIANGVTSK 106
               || ||       ||   :|: |            |: :   :: :| : ::| ||     |:|
Db          19 AFTCL-----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI----TAK 69

Qy         107 VFLAIR-----RCSTFQRMIAEVQEECYSKLNVCSIAKRNP--EAITEVVQLPNHFSNRY 159
               |   |      | : |:|:          |   ||:: :: |  ||:  :  :|    :|
Db          70 VAFIINTDSASRWAIFRRL---------SDSEVCALIEQMPPDEAVWVLDDIP----DRR 116

Qy         160 YNRLVRSLLECDEDTVSTIRDSLMEKIGPNMA------SLFHIL------QTDHCAQTHP 207
               | |::  :   |       |||  ::| | | |         | |             | :::|
Db         117 YRRILELI---DSKKALKIRD--LQKHGRNTAGRLMTNEFFAFLMETTVKDVSACIRSNP 171

Qy         208 RADFNRRRTNEPQKLKVLLRNLRGE 232
                 | |           | : : :||
Db         172 GIDLTR---------LVFVLDFKGE 187


Search completed: April  4, 2006, 14:15:23
Job time : 42 secs
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